



PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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1: <u>CAA70330</u> dioxygenase [Marah

BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

macrocarpus]

```
LOCUS
            CAA70330
                           322 aa
                                                      PLN
                                                                01-MAY-1997
DEFINITION
            dioxygenase [Marah macrocarpus].
            CAA70330
ACCESSION
PID
            q1666096
VERSION
            CAA70330.1 GI:1666096
DBSOURCE
            embl locus MMY09113, accession Y09113.1
KEYWORDS
SOURCE
            Marah macrocarpus.
  ORGANISM
            Marah macrocarpus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
            Rosidae; Cucurbitales; Cucurbitaceae; Marah.
REFERENCE
            1
               (residues 1 to 322)
  AUTHORS
            MacMillan, J., Ward, D.A., Phillips, A.L., Sanchez-Beltran, M.J.,
            Gaskin, P., Lange, T. and Hedden, P.
  TITLE
            Gibberellin biosynthesis from gibberellin A12-aldehyde in endosperm h \in \mathcal{U}_k
            and embryos of Marah macrocarpus
  JOURNAL
            Plant Physiol. 113 (4), 1369-1377 (1997)
  MEDLINE
            97267151
REFERENCE
                (residues 1 to 322)
  AUTHORS
            Hedden, P.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (31-OCT-1996) P. Hedden, University of Bristol,
            Department of Agricultural Sciences, IACR-Long Ashton Research
            Station, Long Ashton, Bristol, BS18 9AF, UK
FEATURES
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                      /db xref="taxon:48242"
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      121 klrsalndyi wavrnmacei velmaeglki qqrnalskll mgeesdsvfr vnhyppcpee
      181 lqalegtnmi gfgehtdpqi isvlrsnnts glqislpdan wisvppdqts ffinvgdslq
      241 vmtngrfksv khrvltnslk srismiyfgg pplsekiapl pslmkgeesl ykeftwfeyk
      301 rsaynsrlad nrlvhferia as
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PubMed Nucleotide			Structure		ranoriering	OMIM
Search Protein V for	71.5			<b>建模型。</b>	SV SV GO G	
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**1:** AAD04293 copalyl diphosphate BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

synthase 2; CPS2 [Cucurbita maxima]

13-JAN-1999 PLN 827 aa LOCUS AAD04293 DEFINITION copalyl diphosphate synthase 2; CPS2 [Cucurbita maxima]. ACCESSION AAD04293 g4151195 PID

AAD04293.1 GI:4151195 VERSION

locus AF049906 accession AF049906.1 DBSOURCE

KEYWORDS

SOURCE winter squash. ORGANISM Cucurbita maxima

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

Cucurbitales; Cucurbitaceae; Cucurbita.

(residues 1 to 827) REFERENCE 1

Smith, M.W., Yamaguchi, S., Ait-Ali, T. and Kamiya, Y. AUTHORS

The first step of gibberellin biosynthesis in pumpkin is catalyzed TITLE

by at least two copalyl diphosphate synthases encoded by

differentially regulated genes

Plant Physiol. 118 (4), 1411-1419 (1998) JOURNAL

MEDLINE 99063778

(residues 1 to 827) REFERENCE

Smith, M.W., Yamaguchi, S., Ait-Ali, T. and Kamiya, Y. AUTHORS

Direct Submission TITLE

Submitted (20-FEB-1998) Plant Hormone Function Lab, Frontier JOURNAL

Research Program, Institute of Physical and Chemical Research

(RIKEN), Hirosawa 2-1, Wako-shi 351-0198, Japan Method: conceptual translation supplied by author.

COMMENT Location/Qualifiers **FEATURES** 

source

/organism="Cucurbita maxima"

/db xref="taxon:3661"

1..827 Protein

/product="copalyl diphosphate synthase 2"

/note="CPS2"

CDS 1..827

/coded by="AF049906.1:1..2484"

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//

```
601 aalvhtiash ykdanahqrr aflqqftnfh aaqpydnnaw rsgnmqqkgg eglvgillrt
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721 llsnsqfqkl snltnkvchq lahfkkhkvn ngnlykektd nkmppeieed irklvqlviq
781 kssdgndids pikqtfltva ksvyyaayfd awtinyhiak vlfervf
```





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Search IPro	ten for		TWANT PA				
		s Inde	X Hist	ory Clipb	া আহত		representation.
<b>1</b> : <u>T0295</u>	9 kaurene sy	nthase A -	maize B	Link, PubMe	d, Related	Sequences, 7	Taxonomy

LOCUS T02959 823 aa PLN 29-OCT-1999

DEFINITION kaurene synthase A - maize.

ACCESSION T02959 PID q7489781

VERSION T02959 GI:7489781 DBSOURCE pir: locus T02959;

summary: #length 823 #molecular-weight 95122 #checksum 392;

genetic: #gene AN1;

PIR dates: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change

29-Oct-1999.

KEYWORDS

SOURCE Zea mays.
ORGANISM Zea mays

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.

REFERENCE 1 (residues 1 to 823)

AUTHORS Bensen, R.J., Johal, G.S., Crane, V.C., Tossberg, J.T., Schnable, P.S.,

Meeley, R.B. and Briggs, S.P.

TITLE Cloning and characterization of the maize Anl gene

JOURNAL Plant Cell 7 (1), 75-84 (1995)

MEDLINE <u>95210929</u>

FEATURES Location/Qualifiers

source 1..823

/organism="Zea mays"
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Protein 1..823

/product="kaurene synthase A"

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PubMed Nucle	,01100 110101		Structure		Taxonomy	OMIM
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A CONSTRUCTION OF THE	ીજાઉં : ા		story Clip	board 🔆		
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1: AAB87091 copalyl BLink, PubMed, Related Sequences, Nucleotide, Taxonomy pyrophosphate synthase [Stevia

rebaudiana]

```
PLN
                                                               22-MAR-2000
            AAB87091
                          787 aa
LOCUS
           copalyl pyrophosphate synthase [Stevia rebaudiana].
DEFINITION
ACCESSION
            AAB87091
            g2642661
PID
VERSION
            AAB87091.1 GI:2642661
            locus AF034545 accession AF034545.1
DBSOURCE
KEYWORDS
            Stevia rebaudiana.
SOURCE
  ORGANISM
           Stevia rebaudiana
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
            II; Asterales; Asteraceae; Asteroideae; Heliantheae; Stevia.
               (residues 1 to 787)
REFERENCE
            Richman, A.S., Gijzen, M., Starratt, A.N., Yang, Z. and Brandle, J.E.
  AUTHORS
            Diterpene synthesis in Stevia rebaudiana: recruitment and
  TITLE
            up-regulation of key enzymes from the gibberellin biosynthetic
            pathway
            Plant J. 19 (4), 411-421 (1999)
  JOURNAL
  MEDLINE
            99435880
   PUBMED
            10504563
REFERENCE
               (residues 1 to 787)
            Richman, A.S., Gijzen, M. and Brandle, J.E.
  AUTHORS
            Direct Submission
  TITLE
            Submitted (13-NOV-1997) Research Branch, Agriculture and Agri-Food
  JOURNAL
            Canada, 1391 Sandford St., London, ON N5V 4T3, Canada
            Method: conceptual translation supplied by author.
COMMENT
                     Location/Qualifiers
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      121 qdvdgsgspq fpsslewian nqlsdgswgd hllfsahdri intlacvial tswnvhpskc
      181 ekglnflren ickledenae hmpigfevtf pslidiakkl nievpedtpa lkeiyarrdi
      241 kltkipmevl hkvpttllhs legmpdlewe kllklqckdg sflfspssta falmqtkdek
      301 clqyltnivt kfnggvpnvy pvdlfehiwv vdrlqrlgia ryfkseikdc veyinkywtk
      361 ngicwarnth vqdiddtamg frvlrahgyd vtpdvfrqfe kdgkfvcfag qstqavtgmf
      421 nvyrasqmlf pgeriledak kfsynylkek qstnelldkw iiakdlpgev gyaldipwya
      481 slprletryy legyggeddv wigktlyrmg yvsnntylem akldynnyva vlqlewytig
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qwyvdigiek fesdniksvl vsyylaaasi feperskeri awakttilvd kitsifdssq 601 sskeditafi dkfrnkssk khsingepwh evmvalkktl hgfaldalmt hsqdihpqlh 661 qawemwltkl qdgvdvtael mvqminmtag rwvskellth pqyqrlstvt nsvchditkl 721 hnfkensttv dskvqelvql vfsdtpddld qdmkqtfltv mktfyykawc dpntindhis 781 kvfeivi
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publied Nucleotide		1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1		
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A A D 20482 ent-kaur	rene Dell'in,			

1: AAB39482 ent-kaurene

synthase B [Cucurbita maxima]

30-DEC-1996 PLN . 789 aa AAB39482 ent-kaurene synthase B. 1.OCUS DEFINITION

AAB39482 ACCESSION g1431870

ÃAB39482.1 GI:1431870 PID VERSION

locus CMU43904 accession U43904.1 DBSOURCE

KEYWORDS

SOURCE ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; winter squash. Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Cucurbita maxima

Cucurbitales; Cucurbitaceae; Cucurbita.

REFERENCE

Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and AUTHORS

Molecular cloning and characterization of a cDNA encoding the TITLE

gibberellin biosynthetic enzyme ent-kaurene synthase B from pumpkin

(Cucurbita maxima L.)

Plant J. 10 (2), 203-213 (1996) JOURNAL

MEDLINE REFERENCE

Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and AUTHORS

TITLE

Submitted (25-DEC-1995) Shinjiro Yamaguchi, The Institute of Physical and Chemical Research, Hirosawa2-1, Wako-shi, Saitama JOURNAL

351-01, Japan

Location/Qualifiers FEATURES

source

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/tissue\_type="immature seeds"

Protein

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biosynthesis"

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/note="terpene cyclase"

ORIGIN

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181 nvdalvrkke lelrscrsns eggkaylayv segigklqdw dmvmqyqrkn gslfnspstt

241 aaafmhrndd gcfdylrsll qkfdgsvpti ypldiyarlh mvdslqkfgi arhfkeeirs

301 vldetyrcwm qgeeniflda stcamafrml rvegydvssd qltqfsedif pnclggylkd

361 fgaslelyka sqiithpdes vleninswts rflkhglssd svwsdrtdsv vkqeavnale 421 fpynatlerl iskramesys gdivrisksp yaclnfghqd flelavedfn tlgrihlkel

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661 gsceyqklyk lmstagrlkn dirsydreck egklnilslw midgggnvtk eeaieaikgd
721 ferairellg lvlqenttip rackdlfwkl msivnlfyme ddgytsnrlm ntvkamfeqp
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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	
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	a contract the state of	Limba Had	SV Hiel		noaro 🔹 💮	WHO WHITE HET OF THE	35-4 37 457 38 52 5
			Marcaga (F) 188	ave Ado	to Clipboard		
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1: AAB58822 ent-kaurene synthase A

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[Pisum sativum]
                                                               05-JUN-1997
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                          801 aa
            AAB58822
LOCUS
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DEFINITION
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ACCESSION
            q2160544
PID
            AAB58822.1 GI:2160544
VERSION
            locus PSU63652 accession U63652.1
DBSOURCE
KEYWORDS
SOURCE
            pea.
  ORGANISM Pisum sativum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
            Fabales; Fabaceae; Papilionoideae; Pisum.
               (residues 1 to 801)
            Ait-Ali, T., Swain, S.M., Reid, J.B., Sun, T.-p. and Kamiya, Y.
REFERENCE
  AUTHORS
            The LS locus of pea encodes the gibberellin biosynthesis enzyme
  TITLE
            ent-kaurene synthase A
            Plant J. 11 (3), 443-454 (1997)
  JOURNAL
            97260958
  MEDLINE
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REFERENCE
            Ait-Ali, T., Swain, S.M., Reid, J.B., Sun, T.-p. and Kamiya, Y.
  AUTHORS
             Direct Submission
  TITLE
             Submitted (12-JUL-1996) Plant Hormone Function, RIKEN Institute,
  JOURNAL
             Hirosawa 2-1, Wako-shi, Saitama 351-01, Japan
             Method: conceptual translation.
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       121 dvnaistpqf psslewiakn qlqdgswgds rlfsahdrii ntlacvialr swnmhsekcd
       181 kgmiffrenl skleneneeh mpigfevafp sllegargik plmcpndspi lknifekrde
       241 kltripkeim hkvpttllhs legmsgldwk qllklqsqdg sflfspssta falmqtkdgn
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       421 nlfrasqvlf pgekilehak hfsakvlkek reanelidkw iimknlpeev gyaldmpwya
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       541 twylesrige fglskrdlli ayflatgsif epersherla wakttallet ikcyvrnedl
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# 1: CAA03884 GTP cyclohydrolase II / BLink, Related Sequences, Nucleotide, synthase [Arabidopsis thaliana]

```
LOCUS -
               CAA03884
                              543 aa
   DEFINITION
               GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phoshate
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               synthase [Arabidopsis thaliana].
   ACCESSION
               CAA03884
   PID
               g2462925
   VERSION
               CAA03884.1 GI:2462925
  DBSOURCE
               embl locus ATAJ0053, accession AJ000053.1
  KEYWORDS
  SOURCE
               thale cress.
    ORGANISM
              Arabidopsis thaliana
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
              Rosidae; Capparales; Brassicaceae; Arabidopsis.
  REFERENCE
                 (residues 1 to 543)
    AUTHORS
              Herz, S.W.
    TITLE
              Direct Submission
    JOURNAL
              Submitted (31-JUL-1997) Herz S.W., Institut fuer Org. Chemie und
              Biochemie, TU Muenchen, Lichtenbergstr. 4, 85747 Garching, FRG
  REFERENCE
                 (residues 1 to 543)
              Herz, S.W., Eberhardt, S. and Bacher, A.
    AUTHORS
    TITLE
              Biosynthesis of riboflavin in plants. The ribA gene of Arabidopsis
              thaliana specifies a bifunctional GTP cyclohydrolase II/
              3,4-dihydroxy-2butanone-4-phosphate synthase
   JOURNAL
              Unpublished
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                       Location/Qualifiers
      source
                       1..543
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                      AJ000053.1:2383..2616)"
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        1 mssinlssss pstislsrsr lsqssttllh glhrvtlpsn hplstfsikt ntgkvkaavi
       61 sreddllsft ngntplsngs liddrteepl eadsvslgtl aadsapapan gfvaedddfe
      121 ldlptpgfss ipeaiedirq gklvvvvdde drenegdlvm aaqlatpeam afivrhgtgi
      181 vcvsmkeddl erlhlplmvn qkeneeklst aftvtvdakh gtttgvsard rattilslas
      241 rdskpedfnr pghifplkyr eggvlkragh teasvdltvl agldpvgvlc eivdddgsma
      301 rlpklrefaa ennlkvvsia dliryrrkrd klverasaar iptmwgpfta ycyrsildgi
      361 ehiamvkgei gdgqdilvrv hsecltgdif gsarcdcgnq lalsmqqiea tgrgvlvylr
      421 ghegrgiglg hklraynlqd agrdtveane elglpvdsre ygigaqiird lgvrtmklmt
      481 nnpakývýlk gyglaivgrv pĺlslitken kryletkrtk mýhmyglkfk gdvvekiese
11
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S NCB	Terrero a constant de la constant de
PubMed	Nucleotide Protein Genome Structure PopSet Taxonomy OMIM
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	Limits Index History Clipboard
Display	efault.View as HTML Save Add to Clipboard
11. AAC39	ent-kaurene BLink, PubMed, Related Sequences, Nucleotide, Taxonomy
_ x. <u>12.100</u> 2	synthase
	[Arabidopsis
	thaliana]
LOCUS DEFINITION ACCESSION PID VERSION	AAC39443 785 aa PLN 17-APR-1998 ent-kaurene synthase [Arabidopsis thaliana]. AAC39443 g3056725 AAC39443.1 GI:3056725
DBSOURCE	locus AF034774 accession AF034774.1
KEYWORDS SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE AUTHORS	1 (residues 1 to 785) Yamaguchi, S., Sun, Tp., Kawaide, H. and Kamiya, Y.
TITLE	The GA2 locus of Arabidopsis thaliana encodes ent-kaurene synthase
JOURNAL MEDLINE	of gibberellin biosynthesis Plant Physiol. 116 (4), 1271-1278 (1998) 98205064
REFERENCE	2 (residues 1 to 785)
AUTHORS TITLE	Yamaguchi, S., Sun, TP., Kawaide, H. and Kamiya, Y. Direct Submission
JOURNAL	Submitted (14-NOV-1997) Botany, Duke University, Research Dr., Durham, NC 27708, USA
COMMENT	Method: conceptual translation supplied by author.
FEATURES	Location/Qualifiers 1785
source	<pre>/organism="Arabidopsis thaliana" /db_xref="taxon:3702" /chromosome="1"</pre>
Protei	/function="terpene cyclase"
900	/product="ent-kaurene synthase"
CDS	/gene="GA2"
ODICIN	/coded_by="AF034774.1:682425"
1 m	sinlrssgc sspisatler gldsevqtra nnvsfeqtke kirkmlekve lsvsaydtsw
61 v 121 g 181 i 241 t 301 t 361 v 421 1 481 w 541 e 601 1	amvpspssq naplfpqcvk wlldnqhedg swgldnhdhq slkkdvlsst lasllakkw igerqinkg lqfielnsal vtdetiqkpt gfdiifpgmi kyardlnlti plgsevvddm rkrdldlkc dsekfskgre aylayvlegt rnlkdwdliv kyqrkngslf dspattaaaf qfgndgclr ylcsllqkfe aavpsvypfd qyarlsiivt leslgidrdf kteiksilde yrywlrgde eicldlatca lafrlllahg ydvsydplkp faeesgfsdt legyvkntfs lelfkaaqs yphesalkkq ccwtkqylem elsswvktsv rdkylkkeve dalafpsyas ersdhrrki lngsaventr vtktsyrlhn ictsdilkla vddfnfcqsi hreemerldr ivenrlqel kfarqklayc yfsgaatlfs pelsdarisw akggvlttvv ddffdvggsk elenlihlv ekwdlngvpe yssehveiif svlrdtilet gdkaftyqgr nvthhivkiw dllksmlre aewssdkstp sledymenay isfalgpivl patyligppl pektvdshqy gllyklystm grllndiggf kresaegkln avslhmkher dnrskeviie smkglaerkr
61 v 121 g 181 i 241 t 301 t 361 v 421 1 481 w 541 e 601 1	/db_xref="taxon:3702" /chromosome="1"  1785 /function="terpene cyclase" /product="ent-kaurene synthase" 1785 /gene="GA2" /coded_by="AF034774.1:682425"  sinlrssgc sspisatler gldsevqtra nnvsfeqtke sylayolegt gfdiifpgmi kyardlnlti plgsevvddm kyardldlkc dsekfskgre aylayvlegt rnlkdwdliv kyarkngslf dspattaaaf qfgndgclr ylcsllqkfe aavpsvypfd qyarlsiivt leslgidrdf kteiksilde eicldlatca lafrlllahg ydvsydplkp faeesgfsdt legyvkntfs rdkylkkeve dalafpsyas ersdhrrki lngsaventr vtktsyrlhn ictsdilkla vdfffcqsi hreemerldr kfarqklayc gysehveiif svlrdtilet gdkaftyqgr nvthhivkiw dallkemlre aewssdkstp sledymenav isfalgpivl patyligppl pektvdshqy

//

781 keslt





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#### 1: <u>AAC31213</u> ethylene receptor homolog BLink, Related Sequences, Nucleotide, Taxonomy [Nicotiana tabacum]

```
LOCUS
            AAC31213
                           762 aa
                                                               16-AUG-1999
                                                     PLN
DEFINITION
            ethylene receptor homolog [Nicotiana tabacum].
ACCESSION
            AAC31213
PID
            q5733831
VERSION
            AAC31213.3 GI:5733831
DBSOURCE
            locus AF026267 accession AF026267.3
KEYWORDS
SOURCE
            common tobacco.
  ORGANISM Nicotiana tabacum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
            I; Solanales; Solanaceae; Nicotiana.
REFERENCE
            1
               (residues 1 to 762)
  AUTHORS
            Zhang, J.-S. and Chen, S.-Y.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (16-AUG-1999) 803 Lab, Institute of Genetics, Academia
            Sinica, Beijing 100101, PRC
  REMARK
            Sequence update by submitter
COMMENT
            On Aug 16, 1999 this sequence version replaced gi:4982466.
            Method: conceptual translation.
FEATURES
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                     /product="ethylene receptor homolog"
     CDS
                     1..762
                     /gene="NTHK1"
                     /coded by="AF026267.3:247..2535"
ORIGIN
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       61 iellyfvscs nfpfkwvlfq fiafivlcgm thllnfwtyy gqhpfqlmla ltifkvltal
      121 vsfataitli tlfpmllkik vrefmlkkkt wdlgrevgli kqqkeagwhv rmltqeirks
      181 ldrhtilytt lvelaktldl hncaiwkpne nktemnlihe lkgrsfssmy nlpiptsdpd
      241 vreikesdgv klldayspla aassggssep gavaairmpm lkvsnfkggt pelvpecyai
      301 lvlvlpgegg rswsngeiei vrvvadgvav alshaavlee sghmretlee gnralggakg
      361 dalrasqarn afqmvmshgl rrpmhsilgl lsllqddnmg ieqrllvdam aktssvvstl
      421 indvmdtstk dnsrfplemr hfqlhsmike aaclakclca hrgynisiev dkslpnyvmg
      481 derrvfqvil hmvgnllkdp nggcltfrvl pesarregid gawktrrshs slenvyirfe
      541 vgssnnhsqp egitstlphc cetrrsreve erlsfsvcrk lvqlmqgdiw vvpnpegfdq
      601 smtvilgfql rpsiavgipe ygessdhshp hsllqgvnvl ladyddvnra vtrklleklg
      661 ctvsavssgh dclgalgpav ssfqivlldl hlpdldgfev tmrirefrsr nwplivgfas
      721 adedvsgrcl qigmngiirk pvllpgiade lqrvllqasi it
11
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	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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#### 1: AAC13635 F6N23.3 gene product [Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS
             AAC13635
                            213 aa
                                                       PLN
                                                                 12-NOV-1999
 DEFINITION F6N23.3 gene product [Arabidopsis thaliana].
 ACCESSION
             AAC13635
 PID
             g3047124
 VERSION
             AAC13635.1 GI:3047124
 DBSOURCE
             locus F6N23 accession AF058919.2
 KEYWORDS
 SOURCE
             thale cress.
   ORGANISM Arabidopsis thaliana
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
             Brassicales; Brassicaceae; Arabidopsis.
 REFERENCE
             1 (residues 1 to 213)
   AUTHORS
             Geisel, C.
   TITLE
             The sequence of A. thaliana F6N23
   JOURNAL
             Unpublished
REFERENCE
             2 (residues 1 to 213)
                                                                               Angles States
  AUTHORS
             Washington University Genome Sequencing Center.
  TITLE
             The A. thaliana Genome Sequencing Project
   JOURNAL
             Unpublished
REFERENCE
             3 (residues 1 to 213)
  AUTHORS
             Waterston, R.
  TITLE
             Direct Submission
             Submitted (10-APR-1998) Department of Genetics, Washington
  JOURNAL
             University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE
             4 (residues 1 to 213)
            Waterston, R.
  AUTHORS
            Direct Submission
  TITLE
  JOURNAL
            Submitted (12-NOV-1999) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
            Method: conceptual translation.
FEATURES
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     source
                      1..213
                      /organism="Arabidopsis thaliana"
                      /cultivar="Columbia"
                      /db xref="taxon:3702"
                      /chromosome="IV"
                      /map="unknown"
                      /clone="F6N23"
     Protein
                      1..213
     CDS
                      1..213
                      /gene="F6N23.3"
                      /coded_by="join(AF058919.2:16976..17111,
                      AF0589\overline{1}9.2:17262..17415, AF058919.2:17785..17889,
                     AF058919.2:18316..18417, AF058919.2:18618..18666,
                     AF058919.2:19056..19151)"
ORIGIN
        1 meiysnhcdt tvyasqalaa asktvetmki vhnfhcyfll vgdinipiiy dvnrlrdgnn
       61 fatrsvdarq kgktiftlfa sfqvscyipe ifhyesldyr nqvateisvp fpidirfcep
      121 nrstkqnksp prcvvafasd lifatislnp hrregmsvaa lsldhsmwfh rpvraddwll
```

181 fvivsptate srgfatgkmf nrkgevrcci eee





	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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☐ 1: <u>AAD31397</u> ethylene

BLink, PubMed, Related Sequences, Nucleotide, Taxonomy

receptor homolog [Lycopersicon esculentum]

```
LOCUS
             AF118844 1
                           767 aa
                                                      PLN
                                                                20-MAY-1999
             ethylene receptor homolog [Lycopersicon esculentum].
DEFINITION
ACCESSION
             AAD31397
PTD
             q4877653
VERSION
             AAD31397.1 GI:4877653
DBSOURCE
             locus AF118844 accession AF118844.1
KEYWORDS
SOURCE
             tomato.
  ORGANISM
            Lycopersicon esculentum
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids
            I; Solanales; Solanaceae; Solanum; Lycopersicon.
REFERENCE
                (residues 1 to 767)
            1
  AUTHORS
            Tieman, D.M. and Klee, H.J.
  TITLE
            Differential expression of two novel members of the tomato
            ethylene-receptor family
  JOURNAL
            Plant Physiol. 120 (1), 165-172 (1999)
  MEDLINE
            99252262
REFERENCE
                (residues 1 to 767)
  AUTHORS
            Tieman, D.M. and Klee, H.J.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (08-JAN-1999) Horticultural Sciences, University of
            Florida, P.O. Box 110690, Gainesville, FL 32611, USA
            Method: conceptual translation supplied by author.
COMMENT
FEATURES
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                     /strain="Rutgers"
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      121 alvscatait lltliplllk ikvrelflag nvleldgevg mmkkgteasm hvrmltheir
      181 ksldkhtily ttlvelsktl klancavwmp nesrsamnlt helspssaae shrslsindp
      241 dvleitknkg vrilrqdsvl aasssggsge pcavaairmp llrasdfkgg tpelvdtrya
      301 ilvlvlssvd ervwsydeme ivevvadqva valshatvle esqtmrekle mrnrvlqqaq
      361 enamkasqar tsfqkvmnng mrrpmhsilg llsifqdeka ssdqrmivdt mvktstvlst
```

421 lindameisa kddgrfpvem kpfqlhllvr easclvkclc vykgfgfstd vptslpnqvm 481 gdekrtfqvl lhmvghllnv sigkgsvifr vvletgaetg ndkvwgtrrp sttdeyvtik 541 feievslegs qsdssistih fggrrhnske vteglsfnmc kklvqmmqgn iwmssnaggh 601 aqgmtlilrf qkqssfrkrm feyrnpleqp isstmfrglh vlltddddvn rlvtrkllek //

```
661 lgcqvtavst gfqclsalgp slttfqvlil dlqmpemdgy evalrvrkfr srswpliial
721 tasseeqvwe kclqvgmngl irkpvllqgl adelqrllqr ggggdgl
```





PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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## 1: AAD26899 ethylene receptor homolog BLink, Related Sequences, Nucleotide, Taxonomy [Phalaenopsis sp. 'True Lady']

```
LOCUS
             AAD26899
                           633 aa
                                                      PLN
                                                                17-JUN-1999
 DEFINITION ethylene receptor homolog [Phalaenopsis sp. 'True Lady'].
ACCESSION
             AAD26899
PID
             q4650821
VERSION
             AAD26899.1 GI:4650821
             locus AF055894 accession AF055894.1
DBSOURCE
KEYWORDS
SOURCE
             Phalaenopsis sp. 'True Lady'.
   ORGANISM
            Phalaenopsis sp. 'True Lady'
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Phalaenopsis.
REFERENCE
               (residues 1 to 633)
  AUTHORS
             Do, Y.Y., Chen, Y.C. and Huang, P.L.
  TITLE
            Molecular Analysis of a cDNA Encoding Ethylene Receptor That
             Expresses in Phalaenopsis Petals (Accession Number AF055894)
             (PGR99-047)
  JOURNAL
            Plant Physiol. 119 (4), 1567 (1999)
REFERENCE
            2 (residues 1 to 633)
  AUTHORS
            Huang, P.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (25-MAR-1998) Horticulture, National Taiwan University,
            No.1, Section 4, Roosevelt Rd, Taipei, Taiwan 10617, Republic of
            China
COMMENT
            Method: conceptual translation.
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       61 fivlcgathl inlwtftmhs rtlaivmtva kvstavvsca talmlvhiip dllsvktrel
      121 flrnkaeeld kemglirtge etgrhvrmlt heirstldrh tilrttlvel grtldlaeca
      181 lwmpsrtgln lqlshtlnnq ipvgsvvsin lpvvnqvfns sravriphtc qlarfqphtg
      241 ryvppevvav rvpllhlsnf qindwpelsa knfavmvlml psdsarkwhv yelelvevva
      301 dqvavalsha aileesmrar dqlmdqnval dlarreaema irarndflav mnhemrtpmh
      361 aiialsslll eteltpeqrl mvetilkssn llatlindvl dlskledgsf elevtvfnlh
      421 tvfrevvnli kpiaavkkls livslspdlp scavgdekrl mqtmlnvvgn avkftkegsi
      481 sitasiakpd slrdprdpef ypipsdghfy lrvqikdtgc gispqelphl ftkfahaqng
      541 sdkgyngsgl glaickrfvn lmkghiwles evlgkgctti fivkvgised pahryqhkll
      601 ppiragqsea dafgskrtpt dliplknryq rsl
11
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	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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## 1: BAA37129 gibberelin BLink, PubMed, Related Sequences, Nucleotide, Taxonom 3beta-hydroxylase [Lactuca sativa]

```
LOCUS
             BAA37129
                            363 aa
                                                      PLN
                                                                 05-FEB-1999
 DEFINITION
             gibberelin 3beta-hydroxylase [Lactuca sativa].
 ACCESSION
             BAA37129
 PID
             a4164145
             BAA37129.1 GI:4164145
 VERSION
             locus AB012205 accession AB012205.1
 DBSOURCE
 KEYWORDS
 SOURCE
             Lactuca sativa.
   ORGANISM
             Lactuca sativa
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
             Asteridae; Asterales; Asteraceae; Lactuca.
 REFERENCE
                (residues 1 to 363)
             1
  AUTHORS
             Toyomasu, T.
             Direct Submission
   TITLE
             Submitted (16-MAR-1998) Tomonobu Toyomasu, Yamagata University,
   JOURNAL
             Faculty of Agriculture; Wakaba-cho 1-23, Tsuruoka, Yamagata
             997-8555, Japan (E-mail:toyomasu@tds1.tr.yamagata-u.ac.jp,
             Tel:81-0235-28-2861, Fax:81-0235-28-2812)
REFERENCE
                (sites)
  AUTHORS
            Toyomasu, T., Kawaide, H., Mitsuhashi, W., Inoue, Y. and Kamiya, Y.
            Phytochrome regulates gibberellin biosynthesis during germination
  TITLE
            of photoblastic lettuce seeds
  JOURNAL
            Plant Physiol. 118 (4), 1517-1523 (1998)
  MEDLINE
             99063790
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                     /product="gibberelin 3beta-hydroxylase"
     CDS
                     1..363
                     /gene="Ls3h1"
                     /coded by="AB012205.1:35..1126"
ORIGIN
        1 mhtrvadafk ahpmvnqkhl dlksmkelpe shawlsqdgs psygsssseq vpvinlkdpn
       61 amklvghack twgvfqvtnh gvptnlleem eaagrklfal piqqklkaar apdgvsgygv
      121 arissffpkl mwsegftiig spyeharklw pnrysrfcdv iegykhemnn lagrlmwlml
      181 gslgvttedv kwdgsqgscp alqlnsypac pdpdramgla ahtdstllti lyqnntsglq
      241 ahregagwvt vppipgalvv nvgdllhils nglypsvlhr amvnrtqhrl svaylygpps
      301 nvqisplskl tdhvhpplyr pvtwseylgt kakhfnkals svrlcvplng fvdandhsgv
      361 pvg
11
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#### ☐ 1: <u>CAA74331</u> **gibberellin 20-oxidase** BLink, Related Sequences, Nucleotide, Taxonomy [Triticum aestivum]

```
LOCUS
             CAA74331
                           365 aa
                                                      PLN
                                                                25-JUN-1997
DEFINITION
             gibberellin 20-oxidase [Triticum aestivum].
ACCESSION
             CAA74331
PID
             g2222798
VERSION
             CAA74331.1 GI:2222798
DBSOURCE
             embl locus TAY14008, accession Y14008.1
KEYWORDS
SOURCE
             Triticum aestivum.
  ORGANISM
             Triticum aestivum
             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
             euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
             Poaceae; Triticum.
REFERENCE
             1 (residues 1 to 365)
  AUTHORS
             Appleford, N.E.
  TITLE
             Direct Submission
  JOURNAL
             Submitted (24-JUN-1997) Appleford N.E., Plant Sciences, IACR-Long
            Ashton Research Station, Dept. of Agricultural Sciences, University
            of Bristol, Long Ashton, Bristol. BS18 9AF UK
REFERENCE
               (residues 1 to 365)
  AUTHORS
            Appleford, N.E.J.
  TITLE
            Cloning and characterisation of cDNAs encoding gibberellin
            20-oxidase from wheat (Triticum aestivum L.)
  JOURNAL
            Unpublished
FEATURES
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                      /clone lib="LambdaZapScut"
                      /dev_stage="germinating grain 3 days at 25 degrees C"
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                     /product="gibberellin 20-oxidase"
     CDS
                     1..365
                     /db xref="SPTREMBL:004706"
                     /coded by="Y14008.1:176..1273"
ORIGIN
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       61 lvgeacerhg ffqvvnhgid aelladahrc vdafftmplp ekqralrrpg escgyassft
      121 grfasklpwk etlsfrscps dpalvvdyiv atlgedhrrl gevyarycse msrlsleime
      181 vlgeslgvgr ahyrrffegn dsimrlnyyp pcqrpmetlg tgphcdptsl tilhqdnvgg
      241 lqvhtegrwr sirpradafv vnigdtfmal sngryksclh ravvnskvpr kslafflcpe
      301 mdkvvappgt lvdaanpray pdftwrslld ftqkhyradm ktlevfsswi vqqqqgqllp
      361 plash
//
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	Nucleotide	Protein		Structure		OMIM
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#### 1: AAB67838 gibberellin 20-oxidase [Pisum sativum]

BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS
             AAB67838
                            379 aa
                                                       PLN
                                                                 28-AUG-1997
             gibberellin 20-oxidase [Pisum sativum].
 DEFINITION
 ACCESSION
             AAB67838
 PID
             q1381673
 VERSION
             AAB67838.1 GI:1381673
 DBSOURCE
             locus PSU58830 accession U58830.1
 KEYWORDS
 SOURCE
             pea.
  ORGANISM
             Pisum sativum
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
             Fabales; Fabaceae; Papilionoideae; Pisum.
REFERENCE
             1 (residues 1 to 379)
             Lester, D.R., Ross, J.J., Ait-Ali, T., Martin, D.N. and Reid, J.B.
  AUTHORS
             A gibberellin 20-oxidase cDNA (Accession no. U58830) from pea seed
  TITLE
             (PGR96-050)
  JOURNAL
             Plant Physiol. 111, 1353 (1996)
REFERENCE
               (residues 1 to 379)
  AUTHORS
             Lester, D.R., Ross, J.J., Ait-Ali, T., Martin, D.N. and Reid, J.B.
  TITLE
             Direct Submission
  JOURNAL
             Submitted (21-MAY-1996) Plant Science, University of Tasmania,
             Churchill Avenue, Hobart, TAS 7005, Australia
COMMENT
            Method: conceptual translation supplied by author.
FEATURES
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                      1..379
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                      /db xref="taxon:3888"
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                      1..379
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ORIGIN
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      181 rqfgivyqky ceamsnlslg imellgmslg vgkeyfreff egnesvmrln yyppcknpdl
      241 afgtgphcdp tsltilhqdq veglqvlvdg iwhsvvpked afvvnigdtf malsngmfks
      301 clhraivndk ivrkslaffl cpnedkivtp pkelidkenp rkypnftwps lleftqkhyr
      361 adertldafs mwlqekttt
//
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<b>Dishia</b>			RI i	nk Related	Sequences	, Nucleotide,	Taxonomy

#### 1: CAB45891 putative protein [Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

PLN

24-JUN-1999

363 aa CAB45891 putative protein [Arabidopsis thaliana]. LOCUS DEFINITION CAB45891 ACCESSION

g5262786 PID

CAB45891.1 GI:5262786 embl locus ATT13K14, accession AL080282.1 VERSION DBSOURCE

KEYWORDS

thale cress. SOURCE

ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Arabidopsis thaliana Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;

Brassicaceae; Arabidopsis.

REFERENCE

(residues 1 to 363) Bevan, M., Pohl, T., Weizenegger, T., Bancroft, I., Mewes, H.W., **AUTHORS** 

Mayer, K. F. X., Lemcke, K. and Schueller, C.

Unpublished JOURNAL

(residues 1 to 363) REFERENCE 2

EU Arabidopsis sequencing, project. **AUTHORS** 

Submitted (24-JUN-1999) MIPS, at the Max-Planck-Institut fuer TITLE JOURNAL

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: schuelle@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,

E-mail: michael.bevan@bbsrc.ac.uk

Information on performance of analysis and a more detailed COMMENT

annotation of this entry and other sequences of chromosomes 3, 4and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.

Location/Qualifiers **FEATURES** 

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/variety="Columbia" /db xref="taxon:3702" /chromosome="4"

1..363 Protein

/product="putative protein"

1..363 CDS

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Synechocystissp., PIR2:S74377~Contains Cytidine and

deoxycytidylate deaminases zinc-binding region signature,

HAEVFALRDAGELAENATAYVSLEPCNHYGRTPPCTEAL"

ORIGIN

1 mrreedvevd dsfymrkcve lakraigcts pnpmvgcviv kdgdivgqgf hpkagqphae 61 vfalrdagel aenatayvsl epcnhygrtp pctealikak vrrvvigmvd pnpivfssgi

121 srlkdagidv tvsveeelck kmnegfihrm ltgkpflalr ysmsvngcll dkigqgasds

181 ggyyskllqe ydaiilsssl sdelssissq eainvsiqpi qiivasnaqq shilasshtv

241 eesgpkvvvf takesvaesg isssgvetvv lekinldsil dycynrglcs vlldlrgnvk 301 dlevilrdgf eqkllqkvii evlpewstkd erqiasmkwl eskhvkdlqs kqlggsvlle

01/30/2001 9:05 AM

NCBI Sequence Viewer

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361 gyf





	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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### 1: <u>AAB72193</u> ethylene responsive factor BLink, Related Sequences, Nucleotide, Taxonomy [Oryza sativa]

```
LOCUS
             AAB72193
                           636 aa
                                                      PLN
                                                                06-OCT-1997
DEFINITION
             ethylene responsive factor [Oryza sativa].
ACCESSION
             AAB72193
PID
             g2281705
VERSION
            AAB72193.1 GI:2281705
DBSOURCE
             locus AF013979 accession AF013979.1
KEYWORDS
SOURCE
             Oryza sativa.
  ORGANISM
            Oryza sativa
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae;
            Oryza.
REFERENCE
             1
               (residues 1 to 636)
  AUTHORS
            Yau, C.P. and Yip, W.K.
  TITLE
            Nucleotide sequence of a full-length cDNA encoding an ethylene
            receptor from rice (Accession No. AF013979) (PGR97-134)
  JOURNAL
            Plant Physiol. 115, 315 (1997)
REFERENCE
               (residues 1 to 636)
  AUTHORS
            Yau, C.P. and Yip, W.K.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (14-JUL-1997) Botany, University of Hong Kong, Pokfulam
            Road, Hong Kong, Hong Kong
COMMENT
            Method: conceptual translation supplied by author.
FEATURES
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                      /db xref="taxon:4530"
     Protein
                     1..636
                     /product="ethylene responsive factor"
     CDS
                     1..636
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                     /coded by="AF013979.1:66..1976"
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       61 fivlcgathl inlwtfttht ktvamvmtva kvstavvsca talmlvhiip dllsvktrel
      121 flknkaeqld remglirtqe etgrhvrmlt heirstldrh tilkttlvel ggtlgleeca
      181 lwmpsrsgss lqlshtlrhq itvgstvsin lpvvnqvfss nrailiphts plarirplag
      241 ryvppevaav rvpllhlsnf qindwpelsa ksyaimvlml psdsarkwhv helelvevva
      301 dqvavalsha aileesmrar dllmeqnval dlarreaema irarndflav mnhemrtpmn
      361 aiialsslll eteltpeqrl mvetvlkssn llatlindvl dlskledgsl eleikafnlh
      421 avfkevmsfi kpiaaikrls vsvmlapdlp lcaigdekrl mqtilnisgn avkftkeghi
      481 tlvasvvkad slrefrtpdf hptasddnfy lkvqikdtgc gispqdlpqv ftkfpqsqpg
      541 gnrgysgsgl glaickrfvt lmgghiwlds egtgrgctvt fviqlgicdn tnayqqklip
      601 lvwpssgdad fvgpvpnapn eekgqaslks ryqrsi
11
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#### Restrictions on Use | Write to the HelpDesk





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#### 1: AAD03598 ethylene response sensor BLink, Related Sequences, Nucleotide, Taxonomy [Vigna radiata]

```
LOCUS
             AAD03598
                           636 aa
                                                      PLN
                                                                10-JAN-1999
 DEFINITION
             ethylene response sensor [Vigna radiata].
ACCESSION
             AAD03598
PID
             q4138853
VERSION
             AAD03598.1 GI:4138853
DBSOURCE
             locus AF098272 accession AF098272.1
KEYWORDS
SOURCE
            mung bean.
  ORGANISM
            Vigna radiata
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
             Fabales; Fabaceae; Papilionoideae; Vigna.
REFERENCE
             1 (residues 1 to 636)
  AUTHORS
            Kim, J.H., Lee, J.-H., Joo, S. and Kim, W.T.
  TITLE
            Structure of a cDNA encoding an ERS1 homolog and induction of its
            mRNA by ethylene in mung bean seedlings
  JOURNAL
            Unpublished
REFERENCE
            2 (residues 1 to 636)
  AUTHORS
            Kim, J.H., Lee, J.-H., Joo, S. and Kim, W.T.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (08-OCT-1998) Biology, Yonsei University, Sinchon dong
            134, Seoul 120-749, Korea
COMMENT
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      181 alwmpsrngl nlqlshtlty hvqvgstvqt nnpivnevfn spramrippt cplarirplv
      241 gryvppevva vrvpllnlsn fqindwpdis aknyaimvli lptdsvrrwr dhelelvdvv
      301 adqvavalsh aaileesmra rdqlmeqnva ldlarreaem aiharndfla vmnhemrtpm
      361 haiialssll leteltpeqr vmietvlkss nvlatlindv ldlsrledgs lelemgkfnl
      421 hgvlgeivel ikpiasvkkl pitlilapdl pthaigdekr ltqtllnvvg navkftkegy
      481 vsirasvakp eslqdwrppe fyptssdghf yirvqvkdsg cgippqdiph lftkfaqsrs
      541 gparpssgag lglaickrfv nlmgghiwie segpgkgsta tfivklgicg npdpsdhqat
      601 trsqaysgsg glarfkpfik deddsgfstr rngrsf
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#### 1: CAB51211 putative protein

BLink, Related Sequences, Nucleotide, Taxonomy

1: <u>CAB51</u>	211 putative protein	
	[Arabidopsis thaliana]	
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	PLN 19-JUL-1999	
LOCUS	ממסאוין וויוסאי	
DEFINITION	putative protein [Arabidopsis thaliana].	
ACCESSION	CAB51211	
PID	g5541706	
	GARS1211 1 GT • 5541706	
VERSION	embl locus ATT21L8, accession AL096860.1	
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KEYWORDS	• •	
SOURCE	thale cress.	
ORGANISM		a;
	Eukaryota; Viridiplantae; Embryophyta, Hacheophyta, prassicales; Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;	
	Magnoliophyta; eudicotyledons; Rosidae, eurosida 11, 11	
	Brassicaceae; Arabidopsis.	
REFERENCE		
	nation P. Wincker, P., Cattorio, 2.7	
AUTHORS	Choisne, N., Robert, C., Blottler, F., Mewes, H.W., Artiguenave, F., Saurin, W., Weissenbach, J., Mewes, H.W., Cabuallar C., Quetier, F., and Salanoubat,	
	Artiguenave, F., Saurin, W., Weissenbach, G., Hewes, H., Mayer, K.F.X., Lemcke, K., Schueller, C., Quetier, F. and Salanoubat,	Μ.
	Mayer, K.F.X., Lemcke, K., Schledfor, C., 2	
JOURNAL	Unpublished	
REFERENCE	2 (residues 1 to 599)	-
AUTHORS	EU Arabidopsis sequencing, project.	
TITLE		
JOURNAL		
JOOKNAL		•
	Biochemie, Am Klopierspitz 10a, b 0212 Marchem.mpg.de Project schuelle@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project schuelle@mips.biochem.mpg.de Project	
,	Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: Marcel Salahoubat and Flancis Queen, Coordinator: 2 rule of the Coordinator: 2 rule	uе
	d'Interet Public, Centre National de Joyanne France;	
	Gaston Cremieux, BP191, 91006 Evry Cedex, France;	
	http://www.genoscope.cns.fr	
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	annotation of this entry and other sequences of ships and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal.	, •
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	/variety= Columbia	
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Prote	in 1599	
•	/product="putative protein"	
CDC	1599	
CDS	/	
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61	malsfrisss splicratls ngdnsrnynt tddallilad dischouged from malsfrisss splicratls ngdnsrnynt tddallilad dischouged from malsfriss split split ngdnsrnynt tddallilad dischouged from malsfriss split ngdnsrnynt ngdnsrnynt tddallilad dischouged from malsfriss split ngdnsrnynt	
121	atssgkvage gylyaqgtkp aealaveaag elsigatayi imepgdonya allvnaplihr giervvvgir hplqhlrgsa irelrshgie vnvlgedfes kvledarksc llvnaplihr	

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361 421 481	spvgdlgmve fepsiiffvk	evmeyfhlrg mtqalnlidv twdlygmwni	ylsilwecgg cyeqvgpdml tiryhttvhv	tlaasaisss vsgflqpipd kwylalskkh	viqigarksi vihkvvafva llpvipseda nllilbokti	vggntvrqdd qkllaskgve pkliggskap tveidpsvdp kankfvgven kckfstyphl vsaektssa
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#### BLink, PubMed, Related Sequences, Taxonomy

```
1: T09672 ent-kaurene synthase B (EC
            2.5.1.-) - winter squash
LOCUS
            T09672
                           789 aa
                                                     PLN
                                                                21-JUL-2000
DEFINITION
            ent-kaurene synthase B (EC 2.5.1.-) - winter squash.
ACCESSION
            T09672
PID
            g7484763
VERSION
            T09672 GI:7484763
DBSOURCE
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            summary: #length 789 #molecular-weight 89361 #checksum 4319;
            PIR dates: 16-Jul-1999 #sequence revision 16-Jul-1999 #text change
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KEYWORDS
            transferase.
SOURCE
            winter squash.
  ORGANISM Cucurbita maxima
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
            Cucurbitales; Cucurbitaceae; Cucurbita.
REFERENCE
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  AUTHORS
            Yamaguchi, S., Saito, T., Abe, H., Yamane, H., Murofushi, N. and
            Kamiya, Y.
  TITLE
            Molecular cloning and characterization of a cDNA encoding the
            gibberellin biosynthetic enzyme ent-kaurene synthase B from pumpkin
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  JOURNAL
            Plant J. 10 (2), 203-213 (1996)
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     181 nvdalvrkke lelrscrsns eggkaylayv segigklqdw dmvmqyqrkn gslfnspstt
     241 aaafmhrndd gcfdylrsll qkfdgsvpti ypldiyarlh mvdslqkfgi arhfkeeirs
     301 vldetyrcwm qgeeniflda stcamafrml rvegydvssd qltqfsedif pnclggylkd
     361 fgaslelyka sqiithpdes vleninswts rflkhglssd svwsdrtdsv vkqeavnale
     421 fpynatlerl iskramesys gdivrisksp yaclnfghqd flelavedfn tlqrihlkel
     481 eelqrwvven kldelkffrl hlgycyfaaa atltdpelhd ariawaqngv lttvvddfyd
     541 gggseeeldn lielvekwdp dgevgycskd veivflalhs tvceigrral vwqgrsvmrn
     601 vidgwlallk vmrkeaewst nkvvpsmgey meqahvsfal gpiilpmlff vgpklseemi
     661 gsceyqklyk lmstagrlkn dirsydreck egklnilslw midgggnvtk eeaieaikgd
     721 ferairellg lvlqenttip rackdlfwkl msivnlfyme ddgytsnrlm ntvkamfeqp
     781 mdldallnk
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	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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## 1: <u>BAA34124</u> 3b-hydroxylase BLink, Related Sequences, Nucleotide, Taxonomy [Lycopersicon esculentum]

```
LOCUS
             BAA34124
                           373 aa
                                                      PLN
                                                                23-MAY-2000
 DEFINITION
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             BAA34124
 PID
             q3834350
 VERSION
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 DBSOURCE
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 KEYWORDS
 SOURCE
             tomato.
  ORGANISM Lycopersicon esculentum
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales;
             Solanaceae; Solanum; Lycopersicon.
REFERENCE
             1 (sites)
  AUTHORS
             Yang, Y.Y., Rebers, M., Toyomasu, T., Kawaide, H., Kaneta, T. and
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  TITLE
             Cloning of two cDNAs encoding gibberellin 3beta-hydroxylase
             (Accession No. AB010991, AB010992) of tomato (Solanum lycopersicum
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  JOURNAL
             Plant Physiol. 118, 1534 (1998)
REFERENCE
             2 (residues 1 to 373)
  AUTHORS
            Yang, Y.Y., Kaneta, T. and Kamiya, Y.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (08-FEB-1998) Yuji Kamiya, Institute of Physical and
            Chemical Research (RIKEN), Plant Functions Laboratory; Hirosawa
            2-1, Wako, Saitama 351-0198, Japan
             (E-mail:ykamiya@postman.riken.go.jp, Tel:81-48-462-9375,
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		BLi	nk, Related S	Sequences	, Mucieotido,	
A D22645 puts	ative		•			

1: AAD22645 putative

#### P-glycoprotein-like protein [Arabidopsis thaliana]

1..1230

/gene="T7B11.9"

CDS

01-APR-1999 putative P-glycoprotein-like protein [Arabidopsis thaliana]. LOCUS DEFINITION AAD22645 ACCESSION g4558552 AAD22645.1 GI:4558552 PID locus AC007138 accession AC007138.1 VERSION DBSOURCE KEYWORDS thale cress. Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; SOURCE Arabidopsis thaliana Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; ORGANISM Brassicales; Brassicaceae; Arabidopsis. Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A., REFERENCE O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K., AUTHORS Parnell, L.D., Dedhia, N.N. and McCombie, W.R. Arabidopsis thaliana BAC T7B11 from chromosome IV near 10 cM TITLE Unpublished JOURNAL Huang, E.N., Nascimento, L., de la Bastide, M., Habermann, K., Vil, M.D., Preston, R.R., Spiegel, L.A., See, L.H., Shah, R., Matero, A., REFERENCE O'Shaughnessy, A., Rodriguez, M., Shekher, M., Swaby, I., Schutz, K., **AUTHORS** Parnell, L.D., Dedhia, N.N. and McCombie, W.R. Submitted (23-MAR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring TITLE JOURNAL Harbor, NY 11724 (residues 1 to 1230) REFERENCE 3 Parnell, L.D. AUTHORS Submitted (01-APR-1999) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring TITLE **JOURNAL** Arabidopsis thaliana BAC T7B11 from chromosome IV near 9.5 cM Method: conceptual translation supplied by author. REMARK COMMENT Location/Qualifiers **FEATURES** 1..1230 /organism="Arabidopsis thaliana" source /cultivar="Columbia" /db\_xref="taxon:3702" /chromosome="IV" /map="near 10 cM" /product="putative P-glycoprotein-like protein" protein

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PubMed	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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### 1: AAF71978 Putative ABC transporter BLink, Related Sequences, Nucleotide, Taxonomy [Arabidopsis thaliana]

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PID
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VERSION
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DBSOURCE
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             Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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  JOURNAL
             Unpublished
REFERENCE
             2
                (residues 1 to 1423)
  AUTHORS
             Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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  TITLE
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            Stanford University, 855 California Avenue, Palo Alto, CA 94304,
            USA
REFERENCE
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            Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
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            and Davis, R.W.
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  TITLE
  JOURNAL
            Submitted (25-MAY-2000) DNA Sequencing and Technology Center,
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COMMENT
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#### 1: AAB63643 ABC transporter (PDR5-like) isolog

[Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

LOCUS AAB63643 1416 aa PLN 22-JUL-1997 DEFINITION ABC transporter (PDR5-like) isolog. ACCESSION AAB63643 PID g2062169 VERSION AAB63643.1 GI:2062169 locus ATAC001645 accession AC001645.1 **DBSOURCE KEYWORDS** SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 (residues 1 to 1416) **AUTHORS** Rounsley, S.D., Lin, X., Ketchum, K.A., Phillips, C.A., Brandon, R.C., Fuhrmann, J.L., White, O., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C. TITLE Arabidopsis thaliana chromosome III BAC T02004 genomic sequence **JOURNAL** Unpublished REFERENCE (residues 1 to 1416) AUTHORS Rounsley, S.D. Direct Submission TITLE Submitted (22-APR-1997) The Institute for Genomic Research, 9712 JOURNAL Medical Center Dr., Rockville, MD 20850, USA REFERENCE 3 (residues 1 to 1416) AUTHORS Rounsley, S.D. TITLE Direct Submission **JOURNAL** Submitted (22-JUL-1997) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA COMMENT Method: conceptual translation. **FEATURES** Location/Qualifiers source 1..1416 organism="Arabidopsis thaliana" /cultivar="Columbia" /db xref="taxon:3702" /chromosome="III" /map="m228"/clone="T02004" Protein 1..1416 /product="ABC transporter (PDR5-like) isolog" CDS 1..1416

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☐ 1: <u>AAD24623</u> putative

BLink, PubMed, Related Sequences, Nucleotide, Genome, Tax

ABC transporter [Arabidopsis

thaliana]

LOCUS AC006919 2 1450 aa PLN 05-APR-2000 DEFINITION putative ABC transporter [Arabidopsis thaliana]. ACCESSION AAD24623 PID q4581139 VERSION AAD24623.1 GI:4581139 DBSOURCE locus AC006919 accession AC006919.5 KEYWORDS SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE (residues 1 to 1450) **AUTHORS** Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D. Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Van Aken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C. TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis **JOURNAL** Nature 402 (6763), 761-768 (1999) 20083487 MEDLINE **PUBMED** 10617197 REFERENCE 2 (residues 1 to 1450) AUTHORS Lin, X. TITLE Direct Submission JOURNAL Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA COMMENT Method: conceptual translation. FEATURES Location/Qualifiers source 1..1450 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db xref="taxon:3702" /chromosome="II" Protein 1..1450 /product="putative ABC transporter" CDS 1..1450 /gene="At2g36380" /coded by="join(AC006919.5:10119..10507,  $AC0069\overline{1}9.5:10609...10729$ , AC006919.5:10984...11157, AC006919.5:11243..11533, AC006919.5:11613..11703, AC006919.5:11793..12693, AC006919.5:12781..12941,

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11
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	i (Limit	s inde	x Histo	ory Clipb	oard		
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### 1: AAF19673 F1N19.11 [Arabidopsis BLink, Related Sequences, Nucleotide, Taxonomy thaliana]

11-OCT-2000 AC009519 7 PLN 1270 aa LOCUS F1N19.11 [Arabidopsis thaliana]. DEFINITION ACCESSION AAF19673 g6633814 PID AAF19673.1 GI:6633814 VERSION locus AC009519 accession AC009519.4 **DBSOURCE** KEYWORDS thale cress. SOURCE Arabidopsis thaliana ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. (residues 1 to 1270) REFERENCE Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., AUTHORS Shinn, P., Tambunga, G., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howng, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R. Genomic sequence for Arabidopsis thaliana BAC F1N19 from chromosome TITLE JOURNAL Unpublished REFERENCE 2 (residues 1 to 1270) AUTHORS Ecker, J.R. Direct Submission TITLE Submitted (26-AUG-1999) Arabidopsis thaliana Genome Center, JOURNAL Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (residues 1 to 1270) REFERENCE AUTHORS Ecker, J.R. Direct Submission TITLE Submitted (14-OCT-1999) Arabidopsis thaliana Genome Center, JOURNAL Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (residues 1 to 1270) REFERENCE Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., AUTHORS Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission TITLE Submitted (23-DEC-1999) Arabidopsis thaliana Genome Center, **JOURNAL** Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA 5 (residues 1 to 1270) REFERENCE Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., AUTHORS Johnson-Hopson, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N.,

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            Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center,
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            Department of Biology, University of Pennsylvania, 38th and
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  JOURNAL
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1261 dykkllqsst

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1: AAA91256 coded for by C. BLink, PubMed, Related Sequences, Nucleotide, Genome, T elegans cDNA yk95g9.3;
Similar to acvl-CoA

thioesterase [Caenorhabditis

elegans]

LOCUS AAA91256 343 aa INV 03-MAR-1996 DEFINITION coded for by C. elegans cDNA yk95g9.3; Similar to acyl-CoA thioesterase.

ACCESSION AAA91256 PID g1213545

VERSION AAA91256.1 GI:1213545

DBSOURCE locus CELF25E2 accession U50197.1

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SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans

Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE 1 (residues 1 to 343)

AUTHORS Wilson, R., Ainscough, R., Anderson, K., Baynes, C., Berks, M., Bonfield, J., Burton, J., Connell, M., Copsey, T., Cooper, J., Coulson, A., Craxton, M., Dear, S., Du, Z., Durbin, R., Favello, A., Fulton, L., Gardner, A., Green, P., Hawkins, T., Hillier, L., Jier, M., Johnston, L., Jones, M., Kershaw, J., Kirsten, J., Laister, N., Latreille, P., Lightning, J., Lloyd, C., McMurray, A., Mortimore, B.,

O'Callaghan, M., Parsons, J., Percy, C., Rifken, L., Roopra, A., Saunders, D., Shownkeen, R., Smaldon, N., Smith, A., Sonnhammer, E., Staden, R., Sulston, J., Thierry-Mieg, J., Thomas, K., Vaudin, M.,

Vaughan, K., Waterston, R., Watson, A., Weinstock, L., Wilkinson-Spread I and Wehldren R.

Wilkinson-Sproat, J. and Wohldman, P.

TITLE 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans

UIDNAT Natura 200 (

JOURNAL Nature 368 (6466), 32-38 (1994)

MEDLINE 94150718

REFERENCE 2 (residues 1 to 343)
AUTHORS Minx, P. and Le, T.

TITLE The sequence of C. elegans cosmid F25E2

JOURNAL Unpublished COMMENT Submitted by:

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA, and Sanger Centre, Hinxton Hall Cambridge CB10 IRQ, England

e-mail: rw@nematode.wustl.edu and jes@sanger.ac.uk NEIGHBORING COSMID INFORMATION:

5' cosmid is T04G9, 650 bp overlap; 3' cosmid is F39H12, 200 bp overlap. Actual start of this cosmid is at base position 26996 of CELT04G9; actual end is at bp 29780 of CELF25E2.

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            the program Genefinder (P. Green and L. Hillier, ms in preparation).
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11
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1: NP 005460 peroxisomal BLink, PubMed, Related Sequences, Nucleotide, Taxonomy, Lin acvl-CoA

thioesterase

Homo

sapiens]

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01-NOV-2000
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REFERENCE
            Liu, L.X., Margottin, F., Le Gall, S., Schwartz, O., Selig, L.,
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            Benarous, R. and Benichou, S.
            Binding of HIV-1 Nef to a novel thioesterase enzyme correlates with
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             Nef-mediated CD4 down-regulation
             J. Biol. Chem. 272 (21), 13779-13785 (1997)
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            Watanabe H, Shiratori T, Shoji H, Miyatake S, Okazaki Y, Ikuta K,
  AUTHORS
             Sato T and Saito T.
             A novel acyl-CoA thioesterase enhances its enzymatic activity by
  TITLE
             direct binding with HIV Nef
             Biochem. Biophys. Res. Commun. 238 (1), 234-239 (1997)
  JOURNAL
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  MEDLINE
             9299485
   PUBMED
                (residues 1 to 319)
REFERENCE
             Jones JM, Nau K, Geraghty MT, Erdmann R and Gould SJ.
  AUTHORS
             Identification of peroxisomal acyl-CoA thioesterases in yeast and
  TITLE
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             J. Biol. Chem. 274 (14), 9216-9223 (1999)
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#### 1: T03439 probable ethylene-response protein - rice BLink, Related Sequences, Taxonomy

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LOCUS
            T03439
                           636 aa
                                                                24-MAR-1999
DEFINITION
            probable ethylene-response protein - rice.
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            q7489538
            T03439 GI:7489538
VERSION
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            genetic: #gene ERS;
            PIR dates: 24-Mar-1999 #sequence revision 24-Mar-1999 #text change
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            Yau, C.P. and Yip, W.K.
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<ul> <li>PubMed</li> </ul>	Nucleotide	Protein	Genome	Structure	PopSet	Taxonomy	OMIM
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### 1: <u>AAC79098</u> putative oxidoreductase BLink, Related Sequences, Nucleotide, Taxonomy [Arabidopsis thaliana]

LOCUS AAC79098 322 aa PLN 24-NOV-1998 putative oxidoreductase [Arabidopsis thaliana]. DEFINITION ACCESSION AAC79098 PID g3924597 VERSION AAC79098.1 GI:3924597 **DBSOURCE** locus AF069442 accession AF069442.1 **KEYWORDS** SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 (residues 1 to 322) **AUTHORS** Parnell, L.D., Gnoj, L., de la Bastide, M., Hameed, A., Habermann, K., Schutz, K., Huang, E., Gottesman, T., Dedhia, N.N. and McCombie, W.R. TITLE Genomic sequence of BAC T4I9 from Arabidopsis thaliana, Chromosome IV, near 16.6 cM **JOURNAL** Unpublished REFERENCE (residues 1 to 322) **AUTHORS** Gnoj, L., Parnell, L.D., de la Bastide, M., Hameed, A., Habermann, K., Schutz, K., Huang, E., Gottesman, T., Dedhia, N.N. and McCombie, W.R. TITLE Direct Submission JOURNAL Submitted (29-MAY-1998) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY 11724, USA Method: conceptual translation supplied by author. COMMENT FEATURES Location/Qualifiers source 1..322 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db xref="taxon:3702" /chromosome="IV" /map="17 cM" /clone="BAC T4I9" Protein 1..322 /product="putative oxidoreductase" CDS 1..322 /gene="T4I9.5" /coded\_by="complement(join(AF069442.1:23721..23969, AF069442.1:24042..24381, AF069442.1:24520..24899))" /note="similar to A. thaliana putative protein F21P8.230, GenBank accession number 3445238; similar to M. domesticus adventitious rooting related oxygenase, GenBank accession

01/30/2001 9:38 43/

functional catalog ID=01.20"

number S57814; similar to P. sativum gibberellin

20-oxidase, GenBank accession number U58830; similar to O. sativa gibberellin C-20 oxidase, GenBank accession number U50333; similar to P. vulgaris gibberellin 20-oxidase, GenBank accession number U70531; most similar to T4I9.6 and T4I9.7; contains Pfam iron/ascorbate family of

oxidoreductases signature position 26 to 287 score=22.4;

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# 1: CAB41036 GA 2-oxidase BLink, PubMed, Related Sequences, Nucleotide, Taxonomy [Phaseolus coccineus]

```
LOCUS
            CAB41036
                           332 aa
                                                                20-APR-1999
                                                     PLN
DEFINITION GA 2-oxidase [Phaseolus coccineus].
ACCESSION
            CAB41036
PID
            q4678586
            CAB41036.1 GI:4678586
VERSION
DBSOURCE
            embl locus PCO132438, accession AJ132438.1
KEYWORDS
SOURCE
            Phaseolus coccineus.
  ORGANISM Phaseolus coccineus
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
            eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
            Phaseolus.
            1 (residues 1 to 332)
REFERENCE
            Thomas, S.G., Phillips, A.L. and Hedden, P.
  AUTHORS
            Molecular cloning and functional expression of gibberellin 2-
  TITLE
            oxidases, multifunctional enzymes involved in gibberellin
            deactivation
  JOURNAL
            Proc. Natl. Acad. Sci. U.S.A. 96 (8), 4698-4703 (1999)
  MEDLINE
            99218343
REFERENCE
            2
                (residues 1 to 332)
            Phillips, A.L.
  AUTHORS
  TITLE
            Direct Submission
  JOURNAL
            Submitted (18-JAN-1999) Phillips A.L., Plant Sciences, IACR Long
            Ashton Research Station, Long Ashton Research Station, Bristol,
            BS41 9AF, UK
FEATURES
                     Location/Qualifiers
     source
                     1..332
                     /organism="Phaseolus coccineus"
                     /db xref="taxon:3886"
                     /tissue_type="Embryo"
                     /dev stage="Late developing seeds"
     Protein
                     1..3\overline{3}2
                     /product="GA 2-oxidase"
     CDS
                     1..332
                     /gene="ga2ox1"
                     /coded by="AJ132438.1:68..1066"
ORIGIN
        1 mvvlsqpaln qffllkpfks tplftgipvv dlthpdaknl ivnacrdfgf fklvnhgvpl
       61 elmanlenea lrffkksqse kdragppdpf gygskrigpn gdvgwveyll lntnpdvisp
      121 kslcifrenp hhfravveny itavknmcya vlelmaeglg irqrntlsrl lkdeksdscf
     181 rlnhyppcpe vqalnrnlvg fgehtdpqii svlrsnstsg lqicltdgtw vsvppdqtsf
      241 finvgdalqv mtngrfksvk hrvladttks rlsmiyfggp alseniaplp svmlkgeecl
      301 ykeftwceyk kaaytsrlad nrlapfqksa ad
//
```





	Nucleotide		Genome	Structure	PopSet	Taxonomy	OMIM
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	a Limit	s : Inde	excent History	ory & Clipb	oard warm		
aDisplays	Default View	⊽as Hil		aver           Add	fo Clipboard		

## 1: T06990 probable giberellin 3beta-dioxygenase (EC BLink, Related Sequences, Taxonomy 1.14.11.15) - wheat

```
LOCUS
             T06990
                           365 aa
                                                      PLN
                                                                20-JUN-2000
DEFINITION
            probable giberellin 3beta-dioxygenase (EC 1.14.11.15) - wheat.
ACCESSION
             T06990
PTD
            q7433220
VERSION
            T06990 GI:7433220
DBSOURCE
            pir: locus T06990;
            summary: #length 365 #molecular-weight 40737 #checksum 4634;
            superfamily: 1-aminocyclopropane-1-carboxylate oxidase;
            PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
            20-Jun-2000.
KEYWORDS
            ascorbic acid; oxidoreductase; seed.
SOURCE
            bread wheat.
  ORGANISM
            Triticum aestivum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; Triticum.
REFERENCE
               (residues 1 to 365)
  AUTHORS
            Appleford, N.E.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (??-JUN-1997) to the EMBL Data Library
FEATURES
                     Location/Qualifiers
     source
                     1..365
                     /organism="Triticum aestivum"
                     /db xref="taxon:4565"
     Protein
                     1..365
                     /product="probable giberellin 3beta-dioxygenase"
                     /EC number="1.14.11.15"
                     /note="gibberellin 20-oxidase"
ORIGIN
        1 mvqpvfdaav lsgradipsq fiwpegespt pdaaeelhvp lidiggmlsg dprataevtr
       61 lvgeacerhg ffqvvnhgid aelladahrc vdafftmplp ekqralrrpg escgyassft
      121 grfasklpwk etlsfrscps dpalvvdyiv atlgedhrrl gevyarycse msrlsleime
      181 vlgeslgvgr ahyrrffegn dsimrlnyyp pcqrpmetlg tgphcdptsl tilhqdnvgg
      241 lqvhtegrwr sirpradafv vnigdtfmal sngryksclh ravvnskvpr kslafflcpe
      301 mdkvvappgt lvdaanpray pdftwrslld ftqkhyradm ktlevfsswi vqqqqgqllp
      361 plash
11
```

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PubMed Nucleotide	. 1010111	Genome	Structure	PopSet	Taxonomy	OMIM
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### 1: AAD52015 unknown [Pisum sativum] BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS
            AF082862 1
                           134 aa
                                                      PLN
                                                                01-SEP-1999
DEFINITION
            unknown [Pisum sativum].
ACCESSION
            AAD52015
PID
            g5813796
VERSION
            AAD52015.1 GI:5813796
DBSOURCE
            locus AF082862 accession AF082862.1
KEYWORDS
SOURCE
            pea.
  ORGANISM
            Pisum sativum
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
            Fabales; Fabaceae; Papilionoideae; Pisum.
REFERENCE
               (residues 1 to 134)
  AUTHORS
            MacKenzie-Hose, A.K., Lester, D.R. and Ross, J.J.
  TITLE
            Seeds, GAs and biosynthesis
  JOURNAL
            Unpublished
REFERENCE
               (residues 1 to 134)
  AUTHORS
            MacKenzie-Hose, A.K., Lester, D.R. and Ross, J.J.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (07-AUG-1998) Plant Science, University of Tasmania, GPO
            Box 252-55, Hobart, Tas 7005, Australia
COMMENT
            Method: conceptual translation.
FEATURES
                     Location/Qualifiers
     source
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                      /organism="Pisum sativum"
                      /db xref="taxon:3888"
                      /dev stage="young seed"
     Protein
                     <1..>134
                     /product="unknown"
     CDS
                     1..134
                     /coded by="AF082862.1:<1..>404"
ORIGIN
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       61 svehrvivnp tqdrvslamf ynpksdliiq pakelvtker palyppmtyd eyrlyirmkg
      121 pcgkaqvesl asqi
11
```

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je <b>Borij</b> e	💓 🔑 Limit	s a kindo	x A Hist	ory a • Clipb	oard*****		
Display 1	Default View :	▼ as HTM	IL 🖟 🗓 S	ave Add	to Clipboard	逐渐失败	

# 1: CAB75931 multi resistance protein homolog [Arabidopsis thaliana] BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS
            CAB75931
                          1490 aa
                                                     PLN
                                                               23-FEB-2000
           multi resistance protein homolog [Arabidopsis thaliana].
DEFINITION
ACCESSION
            CAB75931
            q7076769
PID
VERSION
            CAB75931.1 GI:7076769
DBSOURCE
            embl locus ATT209, accession AL138658.1
KEYWORDS
SOURCE
            thale cress.
            Arabidopsis thaliana
  ORGANISM
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons; core
            eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
            Arabidopsis.
REFERENCE
               (residues 1 to 1490)
            Nyakatura, G., Fartmann, B., Dauner, D., Sterr, W., Holland, R.,
  AUTHORS
            Weichselgartner, M., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F.
            and Salanoubat, M.
  JOURNAL
            Unpublished
REFERENCE
               (residues 1 to 1490)
            EU Arabidopsis sequencing, project.
  AUTHORS
  TITLE
            Direct Submission
  JOURNAL
            Submitted (23-FEB-2000) MIPS, at the Max-Planck-Institut fuer
            Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
            lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
            Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
            d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue
            Gaston Cremieux, BP191, 91006 Evry Cedex, France;
            http://www.genoscope.cns.fr
COMMENT
            Information on performance of analysis and a more detailed
            annotation of this entry and other sequences of chromosomes 3, 4
            and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.
FEATURES
                     Location/Qualifiers
     source
                     1..1490
                     /organism="Arabidopsis thaliana"
                     /variety="Columbia"
                     /db xref="taxon:3702"
                     /chromosome="3"
     Protein
                     1..1490
                     /product="multi resistance protein homolog"
     CDS
                     1..1490
                     /gene="T209.140"
                     /coded_by="complement(join(AL138658.1:61266..61393,
                     AL138658.1:61471..61710, AL138658.1:61800..61863,
                     AL138658.1:61948..62253, AL138658.1:62334..62548,
                     AL138658.1:62631..62925, AL138658.1:63056..63172,
                     AL138658.1:63267..63902, AL138658.1:63991..64077,
                     AL138658.1:64169..66528, AL138658.1:66608..66632))"
                     /note="strong similarity to multi resistance protein mrp
                     Arabidopsis thaliana, EMBL:ATMRPPROT; Contains ABC
```

transporters family signature AA755-769;ATP/GTP-binding

site motif A (P-loop) AA196-203;ATP/GTP-binding site motif A (P-loop) AA665-672;ATP/GTP-binding site motif A (P-loop) AA1273-1280;Prokaryotic membrane lipoprotein lipid attachment site AA459-469;Prokaryotic membrane lipoprotein lipid attachment site AA935-945"

ORIGIN

//

```
1 mfkpfgfaae tgshllttqw lqlgnslclk erisiamqvt flafflihla lkwfgvvrnr
  61 gsndveedlk kqsitvkqsf synisllcsv silgthcfil lllfrdsvvs rcdssvsvfs
 121 aevsqsfswl fvsvvvvkir errlvkfpwm lrswwlcsfi lsfsfdahfi takheplefq
 181 dyadltglla slfllavsir gktgfhlles sgnteplllg dqteqnkkds ysssspygna
 241 tlfqritfsw inplfslgyk rplekddvpd idvkdsarfc shafdqklkt tkekegpgna
 301 ffynsvlryv wrkaainavf avvnastayi gpylindfve flsekqsqsl nhgyllalgf
 361 ltakivetvt qrqwifgarq lglrlraali shiyqkglvl ssqsrqshts qeiinymsvd
 421 vqritdfiwy vnniwmlpiq ifsaiyilqk hlglgalaal vttlmvmacn ypltrlqrny
 481 qsdimnakdd rmkatseilk nmkilklqaw dnqflnkvkt lrkkeydclw kslrlqaftt
 541 filwgapsli svvtfvtcml mgvkltagav lsalatfqml qspifglpdl lsalvqskvs
 601 adriasylqq setqkdavey cskdhtelsv eiengafswe pessrptldd ielkvksgmk
 661 vavcgavgsg kssllssilg eiqklkgtvr vsgkqayvpq spwilsgtir dnilfgsmye
 721 sekyertvka calikdfelf sngdlteige rginmsggqk qriqiaravy qnadiylldd
 781 pfsavdahtg relfedclmg ilkdktvlyv thqveflpaa dlilvmqngr vmqagkfeel
 841 lkqnigfevl vgahnealds ilsiekssrn fkegskddta siaeslqthc dsehnisten
 901 kkkeaklvqd eetekgvigk evylaylttv kggllvpfii laqscfqmlq iasnywmawt
 961 apptaesipk lgmgrillvy allaagsslc vlartilvai gglstaetff srmlcsifra
1021 pmsffdstpt grilnrastd qsvldlemav klgwcafsii qivgtifvms qvawqryytp
1081 tarelsrmsg verapilhhf aeslagatti rafdqrdrfi ssnlvlidsh srpwfhvasa
1141 mewlsfrlnl lshfvfafsl vllvtlpegv inpsiaglgv tyglslnvlq atviwnicna
1201 enkmisveri lqyskipsea plvidghrpl dnwpnvgsiv frdlqvryae hfpavlknit
1261 cefpggkkig vvgrtgsgks tliqalfriv epsqgtivid nvditkiglh dlrsrlgiip
1321 qdpalfdgti rlnldplaqy tdheiweaid kcqlgdvira kderldatvv engenwsvgq
1381 rqlvclgrvl lkksnilvld eatasvdsat dgviqkiinq efkdrtvvti ahrihtvies
1441 dlvlvlsdgr iaefdspakl lqredsffsk likeyslrsn hfagsndlls
```

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BLink, PubMed, Related Sequences, Nucleotide, Taxonomy





		Protein				Taxonomy	OMIM
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	<b>Constitution</b>	sta, Inde	x + Hist	ory Clipb	oad		
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☐ 1: CAA05625 AtMRP4 [Arabidopsis thalianal

LOCUS CAA05625 1516 aa PLN 11-AUG-1998 DEFINITION AtMRP4 [Arabidopsis thaliana].

ACCESSION CAA05625 PID g2959767

VERSION CAA05625.1 GI:2959767

**DBSOURCE** embl locus ATDNAMRP4, accession AJ002584.1

KEYWORDS

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

Rosidae; Capparales; Brassicaceae; Arabidopsis.

REFERENCE (residues 1 to 1516) **AUTHORS** Sanchez-Fernandez, R. TITLE Direct Submission

**JOURNAL** Submitted (05-NOV-1997) Sanchez-Fernandez R., Department of

Genetics, University of Gent (VIB), K.L. Ledeganckstraat 35, 9000

Gent, BELGIUM

REFERENCE (residues 1 to 1516)

Sanchez-Fernandez, R., Ardiles-Diaz, W., Van Montagu, M., Inze, D. and AUTHORS

May, M.J.

TITLE Cloning and expression analyses of AtMRP4, a novel MRP-like gene

from Arabidopsis thaliana

**JOURNAL** Mol. Gen. Genet. 258 (6), 655-662 (1998)

MEDLINE 98334109

**FEATURES** Location/Qualifiers

> source 1..1516

/organism="Arabidopsis thaliana"

/db xref="taxon:3702"

Protein 1..1516

/function="Transport of glutathione-conjugates into the

vacuole"

/product="AtMRP4"

CDS 1..1516

/gene="AtMRP4"

/db xref="SPTREMBL:024525"

/coded by="join(AJ002584.1:1100..3196,

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AJ002584.1:6116..6355, AJ002584.1:6439..6539)"

ORIGIN

1 mwllssspwl selscsysav vehtssvpvp iqwlrfvlls pcpqralfsa vdfifllcfa 61 lhklfsspss sseinghaei rkpligirgr tptrttawfk ttvavtvlls fcsvvlcvla

121 ftgkrrtqrp wnlidplfwl ihavthlvia vlvlhqkrfa alnhplslri ywissfvlts 181 lfavtgifhf lsdaatslra edvasffsfp ltaflliasv rgitglvtae tnsptkpsda

241 vsveksdnvs lyasasvfsk tfwlwmnpll skgykspltl eqvptlspeh kaerlallfe

301 sswpkpsens shpirttllr cfwkeilfta ilaivrlgvm yvgpvliqsf vdftsgkrss

361 pwqgyylvli llvakfvevl tthqfnfdsq klgmlirstl italykkglk ltgsarqnhg

```
421 vgqivnymav daqqlsdmml qlhaiwlmpl qvtvalvlly gslgasvita viqltqvfvf
 481 illgtqrnng yqfslmgnrd srmkatneml nymrvikfqa wenhfnkril kfrdmefgwl
 541 skflysiagn iivlwstpvl isaltfatal algvkldagt vfttttifki lqepirtfpq
 601 smislsqami slgrldsymm skelsedave ralgcdgnta vevrdgsfsw ddednepals
 661 dinfkvkkge ltaivgtvgs gkssllasvl gemhrisgqv rvcgstgyva qtswiengtv
 721 qdnilfglpm vrekynkvln vcslekdlqm mefgdkteig erginlsggq kqriqlarav
 781 yqecdvylld dvfsavdaht gsdifkkcvr galkgktvll vthqvdflhn vdcilvmrdg
 841 kivesgkyde lvssgldfge lvaahetsme lveagadsaa vatsprtpts phassprtsm
 901 esphlsdlnd ehiksflgsh ivedgsklik eeeretgqvs lgvykqycte aygwwgivlv
 961 lffsltwqgs lmasdywlay etsaknaisf dasvfilgyv iialvsivlv sirsyyvthl
1021 glktaqiffr qilnsilhap msffdttpsg rilsrastdq tnvdilipfm lglvvsmytt
1081 İlsifivtcq yawptaffvi plgwlniwyr nyylassrel trmdsitkap iihhfsesia
1141 gymtirsfrk gelfrgenyk ryndnlrmdf hnngsnewlg frlelygswy lcisalfmyl
1201 lpsnvirpen vglslsygls lnsvlffaiy mscfvenkmv sverikqftd ipsesewerk
1261 etlppsnwpf hgnvhledlk vryrpntplv lkgitldikg gekvgvvgrt gsgkstliqv
1321 lfrlvepsgg kiiidgidis tlglhdlrsr fgiipqepvl fegtvrsnid pteqysdeei
1381 wkslercqlk dvvatkpekl dslvvdngen wsvgqrqllc lgrvmlkrsr llfldeatas
1441 vdsqtdaviq kiiredfasc tiisiahrip tvmdqdrvlv idaqkakefd sparllerps
1501 lfaalvqeya lrsagi
```

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BLink, Related Sequences, Nucleotide, Taxonomy





	Nucleotide	Protein				Taxonomy	OMIM
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100	Limit	s Inde	× Hist	ory : Clipb	oard 🚟		
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#### ☐ 1: AAC49791 MRP-like ABC transporter [Arabidopsis thaliana]

```
LOCUS
            AAC49791
                         1515 aa
                                                     PLN
                                                               09-AUG-1997
DEFINITION
           MRP-like ABC transporter [Arabidopsis thaliana].
ACCESSION
            AAC49791
PID
            g2316016
VERSION
            AAC49791.1 GI:2316016
            locus ATU92650 accession U92650.1
DBSOURCE
KEYWORDS
SOURCE
            thale cress.
  ORGANISM
            Arabidopsis thaliana
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
            Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
               (residues 1 to 1515)
```

AUTHORS Tommasini, R., Vogt, E., Schmid, J., Fromentau, M., Amrhein, N. and

Martinoia, E.

TITLE Direct Submission

Submitted (10-MAR-1997) Institut fuer Pflanzenwissenschaften, ETH **JOURNAL** 

Zuerich, Universitaetstrasse 2, Zuerich 8092, Switzerland

Method: conceptual translation supplied by author. COMMENT

FEATURES Location/Qualifiers

source 1..1515

/organism="Arabidopsis thaliana"

/strain="Columbia" /db xref="taxon:3702"

Protein 1..1515

/product="MRP-like ABC transporter" /name="member of the ABC family"

CDS 1..1515

/coded by="U92650.1:17..4564"

ORIGIN

```
1 mdflgsttgs gtlamlfsfs esilpldsrs fllkplflrw lsgflhsvll lvlffswvrk
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 121 gfllgmvswg vlsiclhrcr dcehkkapfl lrlwlvfylv vscyslvvdf vmyerretvp
 181 vhllvfdiva fiaavflgyv avlkkdrsns ngvleeplln ggdsrvggdd svelnktngs
 241 geatpysrag ilslltfswm splidignkk tldledvpql hdtdsvvgla pkfrsmlesp
 301 dggersgvtt fklikalyft aqweilvtaf fafiytvasy vgpalidtfv qylngrrqyn
 361 hegyvlvitf faakivecls qrhwffrlqk vgirmrsalv amiyekgltl scqskqgrts
 421 geiinfmtvd aerignfswy mhdpwmvllq vglalwilyr nlglasiaal vatiivmlin
 481 fpfgrmqerf qeklmeakds rmkstseilr nmrilklqgw emkflskifd lrkseegwlk
 541 kyvynsavis fvfwgaptlv svstfgacil lgiplesgki lsalatfril qepiynlpdt
 601 ismivqtkvs ldrlasylcl dnlqpdiver lpkgssdvav evinstlswd vsssnptlkd
 661 infkvfpgmk vavcgtvgsg kssllssllg evpkvsgslk vcgtkayvaq spwiqsgkie
 721 dnilfgkpme rerydkvlea cslskdleil sfgdqtvige rginlsggqk qriqiaraly
 781 qdadiylfdd pfsavdahtg shlfkevllg llcsksviyv thqveflpaa dlilvmkdgr
 841 isqagkyndi lnsgtdfmel igahqealav vdsvdansvs eksalgqenv ivkdaiavde
 901 klesqdlknd klesvepqrq iiqeeerekg svaldvywky itlayggalv pfillgqvlf
 961 qllqigsnyw mawatpvsed vqapvklstl mivyvalafg sslcillrat llvtagykta
1021 telfhkmhhc ifrspmsffd stpsgrimsr astdqsavdl elpyqfgsva itviqligii
1081 gvmsqvswlv flvfipvvaa siwyqryyia aarelsrlvg vckapliqhf setisgatti
1141 rsfsqefrfr sdnmrlsdvt lgpnsiqlga mewlcfrldm lssltfclfn wfswspiptg
```

```
1201 vidpslagla vtyglslntl qawliwtlcn lenkiisver ilqyasvpse pplviesnrp
1261 eqswpsrgev eirdlqvrya phmplvlrgi tctfkgglrt givgrtgsgk stliqtlfri
1321 vepsageiri dgvniltigl hdlrlrlsii pqdptmfegt mrsnldplee ytddqiweal
1381 dkcqlgdevr kkeqkldssv sengdnwsmg qrqlvclgrv llkrskilvl deatasvdta
1441 tdnliqktlr ehfsdctvit iahrissvid sdmvlllsng iieeydtpvr lledksssfs
1501 klvaeytsrs sssfd
```

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Display : Default Vie	W:   V as   Little		Niels DubMs	ed Related	Sequences,	Taxonomy
TOCACE multida	ma resistance D	rotein 1	SLINK, Publish	50, 110,210	•	

### BLink, PubMed, Related Sequences, Taxonomy 1: T06165 multidrug resistance protein 1 homolog - barley

```
21-JUL-2000
                                                    PLN
            multidrug resistance protein 1 homolog - barley.
                         1232 aa
LOCUS
DEFINITION
            T06165
ACCESSION
            g7442649
PID
            T06165 GI:7442649
            summary: #length 1232 #molecular-weight 134377 #checksum 7107;
VERSION
            pir: locus T06165;
            superfamily: multidrug resistance protein; ATP-binding cassette
DBSOURCE
            PIR dates: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change
             21-Jul-2000.
KEYWORDS
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             barley.
 SOURCE
             Hordeum vulgare
   ORGANISM
             Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
             Davies, T.G., Theodoulou, F.L., Hallahan, D.L. and Forde, B.G.
             Cloning and characterisation of a novel P-glycoprotein homologue
 REFERENCE
   AUTHORS
   TITLE
              from barley
             Gene 199 (\bar{1}-2), 195-202 (1997)
   JOURNAL
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                       Location/Qualifiers
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        181 yfswrlalvs yplvllliip gliygkylly lsresrreya kanslveqal gsiktvysft
         241 aekgiiqryt aildktinlg ikqqiakgla vgftglsfai waflawygsr lvmyhhesgg
         301 riyaagisfv lgglslgmal pelkhfieas vaatrileri nrvpqinddd pkglvldqvr
         361 geiefesirf vypsrpnmtv lkdfnlqipa gqtialvgss gsgkstaial vqrfydaseg
         421 tvkvdgidik klnlksirsk iglvsqdhal fgtsikenil fgkpdatmdl lyaaamtana
         481 hnfimglpeg yetkigerga llsggqkqri aiaravlknp aillldeats aldseseklv
         541 qhaldqasmg rttlvvahkl stvknadqia vvdggriaei gthdelinkg gpysrlvklq
         601 kmvsyidqet dqfrassaar tsasrlsmsr aspmpltpgf sketesyvsp papsfsrlla
         661 mnapewkqal igsisalvyg slqptyalti ggmiaaffvq dhnemnaiis ryalifcsls
         721 lvsiavnllq hynfaymgeh lvrrirvqvl ekiltfeaaw fdedtnssgs lcsrlsdess
         781 lvktlvadri slllqtacgi viavtmgliv awklalvmia vqpctmicyy akkivlsnvs
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```
1141 iaiaraiirn paillldeat saldaqseqv vqealdrimt grttiivahr lntiknadsi
1201 aflgegkvie rgtypqlmnk kgaffnlatl qk
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lence Viewer OMIM Taxonomy Structure Genome ALCO TO CALL OF THE Protein History Choosed . Nucleotide PubMed Search Protein Save La Addito eliptocato al BLink, Related Sequences, Taxonomy Poisplay Default View. 1: T04251 P-glycoprotein 2 - Arabidopsis thaliana 21-JAN-2000 PLNP-glycoprotein 2 - Arabidopsis thaliana. LOCUS DEFINITION summary: #length 1233 #molecular-weight 135209 #checksum 3106; T04251 ACCESSION genetic: #gene pgp2 #map position 4 #introns 81/3; 100/1; 158/3; g7442648 Ť04251 GI:7442648 genetic. #gene pgp2 #map\_position q #incrons 01/3, 100/1, 130/3, 225/3; 312/2; 492/3; 619/2; 752/1; 832/ 3; 915/2; 1053/1; 1166/3 PID VERSION DBSOURCE superfamily: multidrug resistance protein; ATP-binding cassette nomorogy;
PIR dates: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change Arabidopsis thallana
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; 21-Jan-2000. Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; thale cress. KEYWORDS Arabidopsis thaliana SOURCE Bevan, M., Rose, M., Hempel, S., Entian, K.D., Hoheisel, J., Mewes, H.W., Brassicales; Brassicaceae; Arabidopsis. ORGANISM Mayer, K.F.X. and Schueller, C. Submitted (??-MAR-1999) to the Protein Sequence Database REFERENCE AUTHORS Direct Submission Location/Qualifiers TITLE /organism="Arabidopsis thaliana" JOURNAL 1..1233 FEATURES /db\_xref="taxon:3702" source /product="P-glycoprotein 2" 1..1233 /note="protein F20B18.70" protein /regroup mame womarn
/note="ATP-binding cassette homology #label ABC" /region\_name="domain" 379..573 1 mapsgdpape kekemtapkv sllklfsfad fydcvlmtlg svgacihgas vpiffiffgk 1 mapsyapape kekemaapky siikiisiaa iyaavimaiy syyaatiiyas ypiiliitiyk 61 liniiglayl fpkqashrva kysldfvyls vailfsswle vacwmhtger qaakmrrayl Region 121 rsmlsqdisl fdteastgev isaitsdilv vqdalsekvg nflhyisrfi agfaigftsv 181 wqislvtlsi vplialaggi yafvaiglia rvrksyikag eiaeevignv rtvqaftgee 101 wq151vc151 vp11a1ayyi yalvalyila lv1x5yixay elaeevlyiiv hkdiadggks 241 ravrlyreal entykygrka gltkglglgs mhcvlflswa llvwftsvvv hkdiadggks 301 f++mlowica glclggsdd isafwrabaa gwifbmior ntwtbtooks grblgbwdgh ORIGIN 301 fttmlnvvia glslgqaapd isafvrakaa aypifkmier ntvtktsaks grklgkvdgh 361 iqfkdatfsy psrpdvvifd rlnlaipagk ivalvggsgs gkstvislie rfyepisgav
421 lldgppieel dikwlrggig lyngepalfa ttirepilva bddataeeit raableeais 421 lldgnnisel dikwlrgqig lvnqepalfa ttirenilyg kddataeeit raaklseais 481 finnlpegfe tqvgergiql sggqkqriai sraivknpsi llldeatsal daeseksvqe 541 aldrywygrt tyvyahrist vrnadiiavy hegkivefgn henlisnpdg aysslirlqe 601 taslqrnpsl nrtlsrphsi kysrelsrtr ssfcseresv trpdgadpsk kvkvtvgrly our tastqrnpst nittstpnst kystetsitt ssteetesv gwdetqkeik kiailfccas gwdetqkeik vsqalvsyys gwdetqkeik kiailfccas gsqmplfalg vsqalvsyys fdevdrteem laerlaedat ool smirpawmyg vegticaria gsqmpiraig vsqaivsyys gwdelqkelk kialliceas 721 vitlivytie hicfgtmger ltlrvrenmf railkneigw fdevdntssm lasrlesdat 781 liktivvdrs tillqnlglv vtsfiiafil nwrltlvvla typlvisghi seklfmqgyg 841 gdlnkaylka nmlagesvsn irtvaafcae ekilelysre llepskssfr rgqiaglfyg our garmagraa immragesvsh irraarrae ekileryste irepskssir igqragilyg 901 vsqffifssy glalwygstl mdkglagfks vmktfmvliv talamgetla lapdllkgnq

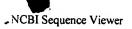
01/30/2001

11

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1081 tiyenilygn egasqsevve samlanahsf itslpegyst kvgergvqms ggqrqriaia
1141 railknpail lldeatsald veservvqqa ldrlmanrtt vvvahrlsti knadtisvlh
1201 ggkiveqgsh rklvlnksgp yfklislqqq qqp
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		s linea	X Hist	ony Cliob	oard VV		
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1: <u>T05802</u> hypothetical protein M7J2.180 - Arabidopsis thaliana

BLink, Related Sequences, Taxonomy

LOCUS T05802 280 aa PLN 17-MAR-2000 DEFINITION hypothetical protein M7J2.180 - Arabidopsis thaliana. ACCESSION T05802 g7486813 PID VERSION T05802 GI:7486813 DBSOURCE pir: locus T05802; summary: #length 280 #molecular-weight 30185 #checksum 9046; genetic: #map\_position 4 #introns 89/3; 119/3; 164/3; 183/3; 202/3 #note M7J2.18 $\overline{0}$ ; superfamily: inner membrane protein malk; ATP-binding cassette homology; PIR dates: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 17-Mar-2000. KEYWORDS SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE (residues 1 to 280) **AUTHORS** Bevan, M., Bargues, M., Perez-Perez, A., Terol, J., Torres, A., Perez-Alonso, M., Hoheisel, J., Mewes, H.W., Mayer, K.F.X. and Schueller, C. Direct Submission TITLE JOURNAL Submitted (??-APR-1998) to the Protein Sequence Database **FEATURES** Location/Qualifiers source 1..280 /organism="Arabidopsis thaliana" /db xref="taxon:3702" Protein  $1..\overline{2}80$ /product="hypothetical protein M7J2.180" ORIGIN 1 msvlmvksdq eklsssyltt afylfhicfs fpcsilssvd vhfayplrpd vkvldglslt 61 lnsgtvtalv gssgagksti vqllarfyep tqgritvgge dvrmfdksew akvvsivnqe 121 pvlfslsvae niayglpneh vskddiikaa kaanahdfii slpqgydtlv gerggllsgg 181 qrqrvaiars llknapilil deatsaldav serlvqsaln rlmkdrttlv iahrlstvqs 241 angiavcsdg kiielgthse lvagkgsyas lvgtgrlafe

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	and a Unite	s de alnde	X Hist		<u>මේල් :                                   </u>	SHEET SHEET	27 in 1
Display.	Default View	as Phili	Le de la s	ave: WAdd	lto Clipboard		

### 1: AAC13635 F6N23.3 gene product BLink [Arabidopsis thaliana]

BLink, Related Sequences, Nucleotide, Taxonomy

```
LOCUS
             AAC13635
                            213 aa
                                                      PLN
                                                                 12-NOV-1999
 DEFINITION
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ACCESSION
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PID
             g3047124
VERSION
             AAC13635.1 GI:3047124
DBSOURCE
             locus F6N23 accession AF058919.2
KEYWORDS
SOURCE
             thale cress.
  ORGANISM Arabidopsis thaliana
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
             Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
                (residues 1 to 213)
  AUTHORS
             Geisel, C.
  TITLE
             The sequence of A. thaliana F6N23
  JOURNAL
             Unpublished
REFERENCE
             2
                (residues 1 to 213)
  AUTHORS
             Washington University Genome Sequencing Center.
  TITLE
             The A. thaliana Genome Sequencing Project
  JOURNAL
             Unpublished
REFERENCE
             3
               (residues 1 to 213)
  AUTHORS
            Waterston, R.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (10-APR-1998) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE
                (residues 1 to 213)
  AUTHORS
            Waterston, R.
            Direct Submission
  TITLE
  JOURNAL
            Submitted (12-NOV-1999) Department of Genetics, Washington
            University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT
            Method: conceptual translation.
FEATURES
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                     AF058919.2:19056..19151)"
ORIGIN
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       61 fatrsvdarq kgktiftlfa sfqvscyipe ifhyesldyr nqvateisvp fpidirfcep
      121 nrstkqnksp prcvvafasd lifatislnp hrregmsvaa lsldhsmwfh rpvraddwll
      181 fvivsptate srgfatgkmf nrkgevrcci eee
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## 1: <u>AAF17668</u> **F20B24.12** [**Arabidopsis** BLink, Related Sequences, Nucleotide, Taxonomy thaliana]

11-OCT-2000 PLN 1316 aa C009398 17 LOCUS F20B24.12 [Arabidopsis thaliana]. DEFINITION ACCESSION AAF17668 g6573748 AAF17668.1 GI:6573748 VERSION locus AC009398 accession AC009398.6 DBSOURCE KEYWORDS thale cress. SOURCE Arabidopsis thaliana ORGANISM Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. (residues 1 to 1316) REFERENCE Shinn, P., Brooks, S., Buehler, E., Chao, Q., Johnson-Hopson, C., AUTHORS Khan, S., Kim, C., Altafi, H., Bei, Q., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzales, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, K., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Federspiel, N.A., Theologis, A. and Ecker, J.R. Genomic sequence for Arabidopsis thaliana BAC F20B24 from TITLE chromosome I Unpublished JOURNAL (residues 1 to 1316) REFERENCE Ecker, J.R. AUTHORS Direct Submission TITLE Submitted (21-AUG-1999) Arabidopsis thaliana Genome Center, JOURNAL Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 3 (residues 1 to 1316) REFERENCE Ecker, J.R. AUTHORS Direct Submission TITLE Submitted (06-NOV-1999) Arabidopsis thaliana Genome Center, JOURNAL Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA (residues 1 to 1316) REFERENCE Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., **AUTHORS** Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L., Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B., Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission TITLE Submitted (14-DEC-1999) Arabidopsis thaliana Genome Center, JOURNAL Department of Biology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, PA 19104-6018, USA (residues 1 to 1316) REFERENCE Chao, Q., Brooks, S., Buehler, E., Johnson-Hopson, C., Khan, S., Kim, C., AUTHORS Shinn, P., Altafi, H., Bei, B., Chin, C., Chiou, J., Choi, E., Conn, L.,

Conway, A., Gonzalez, A., Hansen, N., Howing, B., Koo, T., Lam, B.,

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Lee, J., Lenz, C., Li, J., Liu, A., Liu, J., Liu, S., Mukharsky, N.,
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             Submitted (11-OCT-2000) Arabidopsis thaliana Genome Center,
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      241 ivrvrksyvk aneiaeevig nvrtvqaftg eekavssygg alrntynygr kaglakglgl
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      721 pdwkyglcgt lgsfiagsqm plfalgiaqa lvsyymdwet tqnevkrisi lfccgsvitv
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      841 ivvdrstill enlglvvtaf iisfilnwrl tlvvlatypl iisghisevk rsflrfyilf
      901 fgrqkifmqg yggnlskayl kanmlagesi snirtvvafc aeekvldlys kellepsers
      961 frrgqmagil ygvsqffifs syglalwyiy klfhtkygsi lmekglssfe svmktfmvli
     1021 vtalvmgevl alapdllkgn qmvvsvfell drrtqvvgdt geelsnvegt ielkgvhfsy
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1201 tkvgergiqm sggqrqriai aravlknpei llldeatsal dveservvqq aldrlmrdrt
     1261 tvvvahrlst iknsdmisvi qdgkiieqgs hnilvenkng pysklislqq rqrhhp
//
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	Nucleotide					Taxonomy	
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☐ 1: <u>BAA96612</u> Similar to Arabidopsis

BLink, Related Sequences, Nucleotide, Taxonomy

thaliana chromosome 2, BAC F14M4; putative ABC transporter

(AC004411) [Oryza sativa]

LOCUS BAA96612 1285 aa PLN 10-JUN-2000 DEFINITION Similar to Arabidopsis thaliana chromosome 2, BAC F14M4 ; putative ABC transporter (AC004411) [Oryza sativa].

ACCESSION BAA96612 PID g8468012

VERSION BAA96612.1 GI:8468012

DBSOURCE locus AP002482 accession AP002482.1

KEYWORDS

SOURCE Oryza sativa.
ORGANISM Oryza sativa

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

REFERENCE 1 (residues 1 to 1285)

AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.

TITLE Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC

clone:P0706B05

JOURNAL Published Only in DataBase (2000) In press

REFERENCE 2 (residues 1 to 1285)

AUTHORS Sasaki, T., Matsumoto, T. and Yamamoto, K.

TITLE Direct Submission

JOURNAL Submitted (07-JUN-2000) Takuji Sasaki, National Institute of

Agrobiological Resources, Rice Genome Research Program; Kannondai

2-1-2, Tsukuba, Ibaraki 305-8602, Japan

(E-mail:tsasaki@abr.affrc.go.jp,

URL:http://www.dna.affrc.go.jp:82/, Tel:81-298-38-7441,

Fax:81-298-38-7468)

COMMENT The orientation of the sequence is from T7 to SP6 of the PAC clone.

Genes were predicted from the integrated results of the following: GENSCAN1.0, BLASTN2.0, BLASTX2.0 as well as

SplicePredictor (October 1998 version). The genomic sequence was searched against the non-redundant database NRP (PIR, SWISSPROT, GENPEPT, PDB) from MAFF DNA bank and the cDNA sequence database at RGP. Protein similarities of the coding regions were searched against NRP with BLASTP2.0. ESTs represent the identified cDNA sequences using BLASTN2.0 with the corresponding DDBJ accession no.

and RGP clone ID.

Detailed information on overlap and assembly quality together with

annotation of this entry at

http://www.dna.affrc.go.jp:82/genomicdata/GenomeFinished.html.

FEATURES Location/Qualifiers

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Protein 1..1285

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                     AP002482.1:9642..9908, AP002482.1:9986..10830,
                     AP002482.1:10934..11207, AP002482.1:11317..11842,
                     AP002482.1:12632..12870, AP002482.1:12993..13214,
                     AP002482.1:13312..13487, AP002482.1:13585..13981))"
ORIGIN
        1 mpeswrdaea nasssasvaa adsspgngkg ggggggaava rgeraasasa sarvpfhklf
       61 afadktdaal malgtlgava ngaalpfmtv lfgnlidafg gamgihdvvn rvsmvslefi
      121 ylaiasavas fvqvtcwmit gerqaarirn lylktilrqe iaffdkytnt gevvgrmsgd
      181 tvliqdamge kvgkfiqlvv tflggfivaf aqgwlltlvm matipplvva gavmsnvvak
      241 maslgqaaya essvvveqti gsirtvasft gekqavekyn kslksayksg vreglaaglg
      301 mgtvmvllfc gyslgiwyga klillkgytg akvmnvifav ltgslalgqa spsmkafagg
      361 qaaaykmfet inrkpeiday sttgmkpddi rgdiefrdvy fsyptrpdeq ifrgfslsip
      421 sgttvalvgq sgsgkstvis lierfydpql gdvlidgvnl kefqlrwirs kiglvsqepv
      481 lfaasikeni aygkdnatdq eiraaaelan askfidkmpq gldtsvgehg tqlsggqkqr
      541 iaiarailkd prillldeat saldaeseri vqealdrvmt nrttvivahr lstvrnadti
      601 avihqgtlve kgphhellkd pegaysqlik lqeanrqdks drkgdsgars gkqlsinqsa
      661 srsrrssrdn shhsfsvpfg mplgidiqdg ssdnlcdgmp qdvplsrlas lnkpeipvli
      721 lgsiasvisg vifpifaill snvikafyep phllrkdsqf wssmflvfga vyflslpvss
      781 yĺfsiagcrí ikrirlmtfe kvvnmeiewf dhpenssgai garlsadaak vrglvgdalq
      841 lvvqntttli aglviafvsn welsliilal ipliglngwi qmkfiqgfsa dakmmyeeas
      901 qvandavssi rtvvsfsaee kvmdlykkkc egplrtgirt giisgigfgv sffllfgvya
      961 asfyagarlv eenkttfpkv frvflalama aigvsqsstl tsdsskaksa vssifaivdr
     1021 ksridpseda gvtvetlhgn iefqhvsfry ptrpdveifr dlcltihsgk tvalvgesgs
     1081 gkstaisllq rfydpdvghi lldgvdiqkf qlkwlrqqmg lvsqepalfn dtvraniayg
     1141 kegeatesei ieaaklanah kfissshqgy gttvgergaq lsggqkqria iaraivkdpk
     1201 illldeatsa ldaeservvq daldrymynr ttvivahrls tiqnadliav vkngviiekg
     1261 khdtlmnikd gayaslvalh saass
11
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### 1: <u>CAA75922</u> P-glycoprotein-like protein BLink, Related Sequences, Nucleotide, Taxonomy [Arabidopsis thaliana]

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LOCUS
                           1229 aa
                                                        PLN
                                                                  28-DEC-1997
DEFINITION
             P-glycoprotein-like protein [Arabidopsis thaliana].
ACCESSION
             CAA75922
PID
             q2739309
VERSION
             CAA75922.1 GI:2739309
DBSOURCE
             embl locus ATY15990, accession Y15990.1
KEYWORDS
SOURCE
             thale cress.
  ORGANISM
             Arabidopsis thaliana
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales;
             Brassicaceae; Arabidopsis.
REFERENCE
             1 (residues 1 to 1229)
  AUTHORS
             Sidler, M. and Dudler, R.
  JOURNAL
             Unpublished
REFERENCE
                (residues 1 to 1229)
  AUTHORS
             Dudler, R.
  TITLE
             Direct Submission
  JOURNAL
             Submitted (19-DEC-1997) R. Dudler, University of Zurich, Institute
             of Plant Biology, Zollikerstrasse 107, CH-8008 Zurich, Switzerland
FEATURES
                      Location/Qualifiers
     source
                      1..1229
                      /organism="Arabidopsis thaliana"
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                      1..1229
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                      Y15990.1:3361..3627, Y15990.1:3697..3960,
                      Y15990.1:4113..4409, Y15990.1:4506..4859)"
ORIGIN
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       61 diveivskvc lkfvylglgt lgaaflevac wmitgerqaa rirslylkti lrqdigffdv
      121 etstgevvgr msgdtvlile amgekvgkfi qliatfvggf vlafvkgwll tlvmlvsipl
      181 laiagaampi ivtrassreq aayakastvv eqtlgsirtv asftgekqam ksyrefinla
      241 yrasvkqgfs mglglgvvff vffcsyalai wfggemilkk gytggevvnv mvtvvassms
      301 lgqttpclta faagkaaayk mfetierkps idafdlngkv ledirgeiel rdvcfsypar
     361 pmeevfggfs llipsgataa lvgesgsgks svislierfy dpssgsvlid gvnlkefqlk
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     601 lrdrsinrgs srnirtrvhd ddsvsvlgll grqenteisr eqsrnvsitr iaalnkpett
661 ililgtllga vngtifpifg ilfakvieaf fkpphdmkrd srfwsmifvl lgvaslivyp
     721 mhtylfavag grliqrirvm cfekvvhmev gwfddpenss gtigsrlsad aaliktlygd
```

901 961 1021 1081 1141	vyascfyvga idgksmidsr sgsgkstvis aygkggdeas kepkilllde	aavsgliiaf gsirtvasfc rlvkagrtnf desglvlenv llqrfydpds eaeiiaaael atsaldaese nieggvyasl	ndvfqvflal kgdielchis ghitldrvel anahgfissi	tmtaigisqa ftyqtrpdvq kklqlkwvrq	ikqglisgvg ssfapdsska ifrdlcfair qmglvgqepv	fgisffvlys kgaaasifgi agqtvalvge lfndtirsni
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	Nucleotide					Taxonomy	
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### 1: <u>AAF76889</u> **ABC transporter** BLink, Related Sequences, Nucleotide, Taxonomy, LinkOut [Mus musculus]

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LOCUS
            AF266284 1
                           715 aa
                                                     ROD
                                                               18-JUN-2000
DEFINITION
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ACCESSION
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PID
            g8571454
VERSION
            AAF76889.1 GI:8571454
DBSOURCE
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KEYWORDS
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            house mouse.
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            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
               (residues 1 to 715)
  AUTHORS
            Shirihai, O.S., Gregory, T., Yu, C., Orkin, S.H. and Weiss, M.J.
  TITLE
            ABC-me: A Novel Mitochondrial Transporter Induced by GATA-1 During
            Erythroid Differentiation
  JOURNAL
            EMBO J. (2000) In press
REFERENCE
               (residues 1 to 715)
  AUTHORS
            Shirihai, O., Orkin, S.H., Gregory, T. and Weiss, M.J.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (10-MAY-2000) Hematology-316 ARC, Children's Hospital of
            Philadelphia, 34th and Civic Center Blvd, Philadelphia, PA 19104,
COMMENT
            Method: conceptual translation supplied by author.
FEATURES
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      121 evwkllglvr pergrlsaav gflavssvit msapfflgri idviytnpse gygdsltrlc
      181 avltcvflcg aaangirvyl mqssqqsivn rlrtslfssi lrqevaffdk trtqelinrl
      241 ssdtallgrs vtenlsdglr agaqasvgvg mmffvspsla tfvlsvvppi svlaviygry
      301 lrklskatqd slaeatqlae erignirtir afgkemteve kytgrvdqll qlaqkealar
      361 agffgaagls gnlivlsvly kggllmgsah mtvgelssfl myafwvglsi gglssfysel
      421 mkglgaggrl wellerqprl pfnegmvlde ktfqgalefr nvhftyparp evsvfqdfsl
      481 sipsgsvtal vgpsgsgkst vvslllrlyd pnsgtvsldg hdirqlnpvw lrskigtvsq
     541 epvlfscsva eniaygadnl ssvtaqqver aaevanaaef irsfpqgfdt vvgekgills
      601 ggqkqriaia rallknpkil lldeatsald aenehlvqea ldrlmegrtv liiahrlsti
      661 knanfvavld hgkicehgth eelllkpngl yrklmnkqsf lsyngaeqfl epara
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☐ 1: <u>AAC34225</u> putative

BLink, PubMed, Related Sequences, Nucleotide, Genome, Taxo

**ABC** 

transporter [Arabidopsis thaliana]

LOCUS AAC34225 1286 aa PLN 05-APR-2000 DEFINITION putative ABC transporter [Arabidopsis thaliana]. ACCESSION AAC34225 PTD g3522943 VERSION AAC34225.1 GI:3522943 DBSOURCE locus AC004411 accession AC004411.2 KEYWORDS SOURCE thale cress. ORGANISM Arabidopsis thaliana Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. REFERENCE 1 (residues 1 to 1286) AUTHORS Lin, X., Kaul, S., Rounsley, S.D., Shea, T.P., Benito, M.-I., Town, C.D. Fujii, C.Y., Mason, T.M., Bowman, C.L., Barnstead, M.E., Feldblyum, T.V., Buell, C.R., Ketchum, K.A., Lee, J.J., Ronning, C.M., Koo, H., Moffat, K.S., Cronin, L.A., Shen, M., Van Aken, S.E., Umayam, L., Tallon, L.J., Gill, J.E., Adams, M.D., Carrera, A.J., Creasy, T.H., Goodman, H.M., Somerville, C.R., Copenhaver, G.P., Preuss, D., Nierman, W.C., White, O., Eisen, J.A., Salzberg, S.L., Fraser, C.M. and Venter, J.C. TITLE Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana **JOURNAL** Nature 402 (6763), 761-768 (1999) MEDLINE 20033487 PUBMED 10617197 2 REFERENCE (residues 1 to 1286) **AUTHORS** Lin, X. Direct Submission TITLE **JOURNAL** Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA Method: conceptual translation. COMMENT **FEATURES** Location/Qualifiers source 1..1286 /organism="Arabidopsis thaliana" /cultivar="Columbia" /db xref="taxon:3702" /chromosome="II" Protein 1..1286 /product="putative ABC transporter"

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CDS

1..1286

/gene="At2q47000"

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      241 kaatvveqti gsirtvasft gekqaisnyn khlvtaykag vieggstglg lgtlflvvfc
      301 syalavwygg klildkgytg gqvlniiiav ltgsmslgqt spclsafaag qaaaykmfet
361 ierrpnidsy stngkvlddi kgdielkdvy ftyparpdeq ifrgfslfis sgttvalvgq
      421 sgsgkstvvs lierfydpqa gdvlidginl kefqlkwirs kiglvsqepv lftasikdni
      481 aygkedatte eikaaaelan askfvdklpq gldtmvgehg tqlsggqkqr iavarailkd
      541 prillldeat saldaeserv vqealdrimv nrttvvvahr lstvrnadmi avihqgkive
      601 kgshtellkd pegaysqlir lqeekksden aaeeqkmssi esfkqsslrk sslgrslskg
      661 gssrgnssrh sfnmfgfpag idgnvvqdqe eddttqpkte pkkvsifria alnkpeipvl
      721 ilgsisaaan gvilpifgil issvikaffq ppkklkedts fwaiifmvlg fasiiaypaq
      781 tfffaiagck lvqrirsmcf ekvvhmevgw fdepenssgt igarlsadaa tirglvgdsl
      841 aqtvqnlssi lagliiafla cwqlafvvla mlplialngf lymkfmkgfs adakkmygea
      901 sqvandavgs irtvasfcae dkvmnmyskk cegpmkngir qgivsgigfg fsffvlfssy
      961 aasfyvgarl vddgkttfds vfrvffaltm aamaisgsss lspdsskadv aaasifaimd
     1021 reskidpsve sgrvldnvkg dielrhvsfk yparpdvqif qdlclsirag ktvalvgesg
     1081 sgkstviall qrfydpdsge itldgveiks lrlkwlrqqt glvsqepilf netiraniay
     1141 gkggdasese ivssaelsna hgfisglqqg ydtmvgergi qlsggqkqrv aiaraivkdp
     1201 kvllldeats aldaeservv qdaldrvmvn rttivvahrl stiknadvia vvkngvivek
     1261 gkhdtlinik dgvyaslvql hltaas
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1: CAB83120 ABC transporter-like protein [Arabidopsis

BLink, Related Sequences, Nucleotide, Taxonomy

thaliana] 29-MAR-2000 1539 aa ABC transporter-like protein [Arabidopsis thaliana]. CAB83120 LOCUS DEFINITION CAB83120 ACCESSION g7362750 PID CAB83120.1 GI:7362750 embl locus ATF26K9, accession AL162651.1 VERSION **DBSOURCE** KEYWORDS thale cress. SOURCE Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Arabidopsis thaliana ORGANISM Magnoliophyta; eudicotyledons; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(residues 1 to 1539) REFERENCE

Bloecker, H., Mewes, H.W., Rudd, S., Lemcke, K., Mayer, K.F.X., **AUTHORS** 

Quetier, F. and Salanoubat, M.

Unpublished **JOURNAL** 

(residues 1 to 1539) 2 REFERENCE

EU Arabidopsis sequencing, project. AUTHORS

Submitted (29-MAR-2000) MIPS, at the Max-Planck-Institut fuer TITLE JOURNAL

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail: lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de Project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue

Gaston Cremieux, BP191, 91006 Evry Cedex, France;

http://www.genoscope.cns.fr

Information on performance of analysis and a more detailed COMMENT

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.

Location/Qualifiers **FEATURES** 

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AL162651.1:46127..46213, AL162651.1:46291..48702))" /note="strong similarity to glutathione-conjugate

transporter AtMRP4 - Arabidopsis thaliana,

EMBL: AJ002584~Contains ABC transporters family signature

AA764-778; ATP/GTP-binding site motif A (P-loop) AA674-681; ATP/GTP-binding site motif A (P-loop)

AA1331-1338"

NCBI Sequence Viewer

//

#### ORIGIN

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 181 gilhllsddp aaaslraddv asfisfplta vlllvsikgs tgvvvttsnv tapaksndvv
 241 veksenvsly asasfisktf wlwmnpllrk gyksplnldq vptlspehra eklatlfesk
 301 wpkpqensrn pvrttlircf wkeiaftavl aiirlsviyv gpvliqsfvd ftsgkrssps
 361 qgyylvlill iakfvevlst hqfnfnsqkl gmlirstlit alykkglklt gsarqnhgvg
 421 qivnymavda qqlsdmmlql haiwlmplqv aaaivllynt lgpsvvttvi gltgifvfil
 481 lgtkrnnryg fslmmnrdsr mkatnemlny mrvikfqawe dhfnerilkf remefgwlsk
 541 flysiagnii vlwstpvlis altfttavfl gvkldagtvf ttttifkilq epirtfpqsm
 601 islsqamisl grldaymmsr elseetvers qgcdgnvave ikdgsfswdd eddepaieni
 661 nfevkkgela aivgtvgsgk ssllasvlge mhklsgkvrv cgttayvaqt swiqngtvqd
 721 nilfglpmnr skynevlkvc clekdmqime fgdqteiger ginlsggqkq riqlaravyq
 781 esdvyllddv fsavdahtgs difkkcvrga lkgktillvt hqvdflhnvd rilvmrdgmi
 841 vqsgkydelv ssgldfgelv aahetsmelv eagsasataa nvpmaspitq rsisiesprq
 901 pkspkvhrtt smesprvlrt tsmesprlse lndesiksfl gsnipedgsr likeeerevg
 961 qvsfqvykly steaygwwgm ilvvffsvaw qaslmasdyw layetsakne vsfdatvfir
1021 vyviiaavsi vlvclrafyv thlglktaqi ffkqilnslv hapmsffdtt psgrilsras
1081 tdqtnvdifi pfmiglvatm yttllsifiv tcqyawptvf fiiplgwlni wyrgyylass
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1501 vlvidagkak eydspvrlle rqslfaalvq eyalrsagi
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Display	Default View	▼ as : HTM	IL , , , , S	ave a Add	l to Clipboard		

# 1: <u>CAA72120</u> multi resistance protein BLink, Related Sequences, Nucleotide, Taxonomy [Arabidopsis thaliana]

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                          1514 aa
                                                                19-MAR-1998
                                                      PLN
DEFINITION multi resistance protein [Arabidopsis thaliana].
ACCESSION
            CAA72120
PID
            g2980641
VERSION
            CAA72120.1 GI:2980641
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REFERENCE
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  AUTHORS
            Weigmann, N., Ansorge, M. and Meuller-Roeber, B.
  JOURNAL
            Unpublished
REFERENCE
            2
               (residues 1 to 1514)
  AUTHORS
            Weigmann, N.
  TITLE
            Direct Submission
  JOURNAL
            Submitted (14-FEB-1997) N. Weigmann, MPI of Molecular Plant
            Physiology, Mueller-Roeber, Karl-Liebknechtstr.25, Haus 20, 14476
            Golm, FRG
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      121 lawfvlsflv lhlkykssek lpflvriwwf lafsiclctm yvdgrrlaie gwsrcsshvv
      181 anlavtpalg flcflawrgv sgiqvtrsss dlqepllvee eaaclkvtpy staglvslit
      241 lswldpllsa gskrplelkd ipllaprdra kssykvlksn wkrcksenps kppslaraim
      301 ksfwkeaacn avfaglntlv syvgpylisy fvdylggkei fphegyvlag ifftskliet
      361 vttrqwymgv dilgmhvrsa ltamvyrkgl klssiakqnh tsgeivnyma vdvqrigdys
      421 wylhdiwmlp mqivlalail yksvgiaava tlvatiisil vtiplakvqe dyqdklmtak
      481 dermrktsec lrnmrvlklq awedryrvrl eemreeeygw lrkalysqaf vtfifwsspi
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601 qeeelqedat vviprglsni aieikdgvfc wdpfssrptl sgiqmkvekg mrvavcgtvg 661 sgkssfisci lgeipkisge vricgttgyv sqsawiqsgn ieenilfgsp mektkyknvi 721 qacslkkdie lfshgdqtii gerginlsgg qkqrvqlara lyqdadiyll ddpfsaldah 781 tgsdlfrdyi lsalaektvv fvthqveflp aadlilvlke griiqsgkyd dllqagtdfk 841 alvsahheai eamdipspss edsdenpird slvlhnpksd vfendietla kevqeggsas //

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901 dlkaikekk kakrsrkkql vqeeervkgk vsmkvylsym gaaykgalip liilaqaafq 961 flqiasnwwm awanpqtegd eskvdptlll ivytalafgs svfifvraal vatfglaaaq 1021 klflnmlrsv frapmsffds tpagrilnrv sidqsvvdld ipfrlggfas ttiqlcgiva 1081 vmtnvtwqvf llvvpvavac fwmqkyymas srelvrivsi qkspiihlfg esiagaatir 1141 gfgqekrfik rnlylldcfv rpffcsiaai ewlclrmell stlvfafcmv llvsfphgti 1201 dpsmaglavt yglnlngrls rwilsfckle nkiisieriy qysqivgeap aiiedfrpps 1261 swpatgtiel vdvkvryaen lptvlhgvsc vfpggkkigi vgrtgsgkst liqalfrlie 1321 ptagkitidn idisqiglhd lrsrlgiipq dptlfegtir anldpleehs ddkiwealdk 1381 sqlgdvvrgk dlkldspvle ngdnwsvgqr qlvslgrall kqakilvlde atasvdtatd 1441 nliqkiirte fedctvctia hriptvidsd lvlvlsdgrv aefdtparll edkssmflkl 1501 vteyssrstg ipel
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## 1: T00961 hypothetical protein F20D22.11 - Arabidopsis thaliana

BLink, Related Sequences, Taxonomy

LOCUS T00961 1355 aa PLN 04-MAR-2000
DEFINITION hypothetical protein F20D22.11 - Arabidopsis thaliana.
ACCESSION T00961
PID 97485868
VERSION T00961 GI:7485868
DBSOURCE pir: locus T00961;
summary: #length 1355 #molecular-weight 150282 #checksum 1632;

genetic: #gene ATSP:F20D22.11 #map\_position 1 #introns 521/3; 628/3; 657/3; 890/3; 945/3; 1044/1; 1115/3; 1217/3; 1239/1; 1319/1; superfamily: human multidrug resistance protein cMOAT2; ATP-binding

cassette homology;

PIR dates: 12-Feb-1999 #sequence\_revision 12-Feb-1999 #text\_change

04-Mar-2000.

KEYWORDS

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 1355)

AUTHORS Vysotskaia, V.S., Osborne, B.I., Schwartz, J.R., Toriumi, M., Kwan, A.,

Yu,G., Oji,O., Liu,S., Li,J., Hoang,L., Araujo,R., Au,M., Brendel,V., Buehler,E., Conway,A.B., Conway,A.R., Dewar,K., Feng,J., Kim,C., Kurtz,D., Li,Y., Palm,C.J., Shinn,P., Sun,H.,

Davis, R.W., Ecker, J.R., Federspiel, N.A. and Theologis, A.

TITLE Direct Submission

JOURNAL Submitted (??-MAY-1998) to the EMBL Data Library

FEATURES Location/Qualifiers

source 1..1355

/organism="Arabidopsis thaliana"

/db xref="taxon:3702"

Protein 1..1355

/product="hypothetical protein F20D22.11"

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961 iqkspiihlf gesiagaati rgfgqekrfi krnlylldcf vrpffcsiaa iewlclrmel

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1321 vaefdtparl ledkssmflk lvteyssrst gipel
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	Nucleotide					Taxonomy	OMIM
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☐ 1: AAD25615 Similar to

BLink, Related Sequences, Nucleotide, Taxonomy

ABC-transporter atp-binding protein [Arabidopsis thaliana]

LOCUS C005287\_17 514 aa PLN 10-DEC-1999
DEFINITION Similar to ABC-transporter atp-binding protein [Arabidopsis

thaliana]. AAD25615

ACCESSION AAD25615 PID g4585979

VERSION AAD25615.1 GI:4585979

DBSOURCE locus AC005287 accession AC005287.4

KEYWORDS

SOURCE thale cress.

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1 (residues 1 to 514)

AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vysotskaia, V.S.,

Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

JOURNAL Unpublished

REFERENCE 2 (residues 1 to 514)

AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Kurtz, D.B., Conway, A.R., Au, M., Araujo, R., Buehler, E., Dewar, K., Feng, J., Kim, C., Li, Y., Oji, O., Osborne, B.I., Shinn, P., Sun, H., Toriumi, M., Vyotskaia, V.,

Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (15-JUL-1998) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 3 (residues 1 to 514)

AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V., Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (09-MAR-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304, USA

REFERENCE 4 (residues 1 to 514)

AUTHORS Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F., Altafi, H., Araujo, R., Huizar, L., Rowley, D., Buehler, E., Dunn, P., Gonzalez, A., Kremenetskaia, I., Kim, C., Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P., Toriumi, M., Vyotskaia, V.,

Walker, M., Yu, G., Ecker, J., Theologis, A. and Davis, R.W.

TITLE Direct Submission

JOURNAL Submitted (17-APR-1999) DNA Sequencing and Technology Center, Stanford University, 855 California Avenue, Palo Alto, CA 94304,

USA

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REFERENCE
                (residues 1 to 514)
             Federspiel, N.A., Palm, C.J., Conway, A.B., Conn, L., Hansen, N.F.,
  AUTHORS
             Altafi, H., Araujo, R., Huizar, L., Rowley, D., Brooks, S., Buehler, E.,
             Chao, Q., Dunn, P., Gonzalez, A., Khan, S., Kremenetskaia, I., Kim, C.,
             Lenz, C., Li, J., Liu, S., Luros, S., Schwartz, J., Shinn, P.,
             Toriumi, M., Vyotskaia, V., Yu, G., Ecker, J., Theologis, A. and
             Davis, R.W.
  TITLE
             Direct Submission
             Submitted (10-DEC-1999) DNA Sequencing and Technology Center,
  JOURNAL
             Stanford University, 855 California Avenue, Palo Alto, CA 94304,
COMMENT
             Method: conceptual translation supplied by author.
FEATURES
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                      /cultivar="Columbia"
                      /db xref="taxon:3702"
                      /chromosome="I"
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     CDS
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                      /gene="F20D21.17"
                      /coded by="join(AC005287.4:59053..59322,
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                      AC005287.4:60477..60718, AC005287.4:60796..60878,
                      AC005287.4:60941..61035, AC005287.4:61195..61445,
                      AC005287.4:61534..61743)"
ORIGIN
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       61 nilftiyppl flvlllysfg gtaisvflgk glvnlnflqe kkeadfrysl vrvrenaesi
      121 afyggeqnem qlllqrfrsa fdnltellia srnlefftdg yryliqilpv avvapmyfsg
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      241 deieltyqse mnsslldtng siksqpnqkr leieeltlqt ptngttlvhn lsadvydkdh
      301 llimgpsgsg ktsllramag lwrsgkgkit ekrrrivpst kalygsgifa saialsylec
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1: T06091 hypothetical pro-	22-OCT-1333

1: T06091 hypothetical protein T5J17.20 -Arabidopsis thaliana

LOCUS DEFINITION ACCESSION PID VERSION

DBSOURCE

hypothetical protein T5J17.20 - Arabidopsis thaliana. PLN

T06091 g7487703 T06091 GI:7487703

summary: #length 1383 #molecular-weight 154829 #checksum 8482; genetic: #gene ATSP:T5J17.20 #map\_position 4 #introns 21/2; 116/3; pir: locus T06091; 191/3; 257/3; 409/2; 454/3; 481/1; 558/3; 660/ 2; 704/3; 756/3;

831/1; 867/2; 897/3; 953/3; 992/2; 1070/3; 1131/1; 1198/1; 1247/1;

PIR dates: 30-Apr-1999 #sequence\_revision 30-Apr-1999 #text\_change 22-Oct-1999.

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; thale cress. Arabidopsis thaliana

Brassicales; Brassicaceae; Arabidopsis.

Bevan, M., Murphy, G., Ridley, P., Hudson, S., Bancroft, I., Mewes, H.W., REFERENCE Mayer, K.F.X. and Schueller, C. AUTHORS

Submitted (??-MAR-1999) to the Protein Sequence Database TITLE Location/Qualifiers

JOURNAL **FEATURES** 

source

/organism="Arabidopsis thaliana"

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/product="hypothetical protein T5J17.20"  $1..\overline{1}383$ Protein

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241 awrlcsyasp kyifwilayv lgagtairnf spsfgklmsk eqqlegeyrq lhsrlrthse
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1381 sll
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☐ 1: AAD03441 contains similarity to

BLink, Related Sequences, Nucleotide, Taxonomy

Guillardia theta ABC transporter (GB:AF041468) [Arabidopsis thaliana]

LOCUS AAD03441 557 aa

PLN 10-AUG-1999

DEFINITION contains similarity to Guillardia theta ABC transporter

(GB:AF041468) [Arabidopsis thaliana].

ACCESSION AAD03441 q4115931 PID

VERSION AAD03441.1 GI:4115931

locus T4B21 accession AF118223.2 **DBSOURCE** 

KEYWORDS

thale cress. SOURCE

Arabidopsis thaliana ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

1 (residues 1 to 557) REFERENCE

Abbott, A., Kock, J. and Lehnert, L. AUTHORS The sequence of A. thaliana T4B21 TITLE

JOURNAL Unpublished

REFERENCE (residues 1 to 557)

AUTHORS Washington University Genome Sequencing Center.

The A. thaliana Genome Sequencing Project TITLE

**JOURNAL** Unpublished

REFERENCE (residues 1 to 557)

**AUTHORS** Waterston, R. TITLE

Direct Submission

**JOURNAL** Submitted (06-JAN-1999) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE (residues 1 to 557)

AUTHORS Waterston, R.

TITLE Direct Submission

**JOURNAL** Submitted (06-AUG-1999) Department of Genetics, Washington

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

REFERENCE (residues 1 to 557) 5

Waterston, R. AUTHORS

TITLE Direct Submission

Submitted (10-AUG-1999) Department of Genetics, Washington JOURNAL

University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT Method: conceptual translation.

**FEATURES** Location/Oualifiers

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/clone="T4B21"

1..557 Protein

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      541 gaevnqlmsi klegsvg
11
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1: AAD04949 putative ethylene response BLink, Related Sequences, Nucleotide, Taxonomy sensor [Phalaenopsis sp. 'KCbutterfly']

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LOCUS
             AAD04949
                            633 aa
                                                        PLN
                                                                   14-JAN-1999
 DEFINITION
             putative ethylene response sensor [Phalaenopsis sp. 'KCbutterfly'].
 ACCESSION
             AAD04949
 PID
             g4154359
 VERSION
             AAD04949.1 GI:4154359
 DBSOURCE
             locus AF113541 accession AF113541.1
 KEYWORDS
 SOURCE
             Phalaenopsis sp. 'KCbutterfly'.
             Phalaenopsis sp. 'KCbutterfly
   ORGANISM
             Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
             Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Phalaenopsis.
 REFERENCE
                 (residues 1 to 633)
             Chai, I.J., Lee, B.H., Wang, W.K., Liang, C.C. and Lin, C.Y. Molecular cloning of the Phalaenopsis sp. 'KCbutterfly' ethylene
   AUTHORS
   TITLE
             response sensor cDNA
   JOURNAL
             Unpublished
REFERENCE
             2
                 (residues 1 to 633)
  AUTHORS
             Chai, I.J., Lee, B.H., Wang, W.K., Liang, C.C. and Lin, C.Y.
   TITLE
             Direct Submission
             Submitted (14-DEC-1998) King Car Food Industrial Co. LTD.,
   JOURNAL
             Yuan-Shan Research Institute, 86 Chin-Hsiang Road, Yuan Shan, I-Lan
             264, Taiwan, R.O.C.
COMMENT
             Method: conceptual translation supplied by author.
FEATURES
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PLN ethylene receptor CS-ETR2 [Cucumis sativus].

30-MAY-2000

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KEYWORDS

SOURCE cucumber.

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Cucurbitaceae; Cucumis.

REFERENCE 1 (sites)

AUTHORS Yamasaki, S., Fujii, N. and Takahashi, H.

TITLE The ethylene-regulated expression of CS-ETR2 and CS-ERS genes in cucumber plants and their possible involvement with sex expression

in flowers

JOURNAL Plant Cell Physiol. 41 (5), 608-616 (2000)

MEDLINE 20383769

REFERENCE (residues 1 to 767)

**AUTHORS** Yamasaki, S., Fujii, N. and Takahashi, H.

TITLE Direct Submission

**JOURNAL** Submitted (21-APR-1999) Seiji Yamasaki, Institute of Genetic

Ecology, Tohoku University; Katahira 2-1-1 Aoba-ku, Sendai, Miyagi

980-8577, Japan (E-mail:yamasaki@bansui.ige.tohoku.ac.jp,

Tel:81-22-217-5715(ex.5715), Fax:81-22-263-9845)

**FEATURES** Location/Qualifiers

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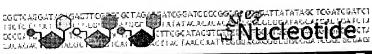


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            Kobayashi, M., Sugiyama, M. and Yamamoto, K.
  AUTHORS
  TITLE
            Isolation of cDNAs encoding GTP cyclohydrolase II from Arabidopsis
  JOURNAL
            Gene 160 (2), 303-304 (1995)
  MEDLINE
            95369709
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COMMENT
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            the EMBL outstation - the European Bioinformatics Institute.
            The original entry is available from http://www.expasy.ch/sprot
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1: U92650 Arabidopsis thaliana MRP-like PubMed, Protein, Related Sequences, Taxonomy ABC transporter mRNA, complete cds

09-AUG-1997 PLN 4809 bp mRNA LOCUS ATU92650 Arabidopsis thaliana MRP-like ABC transporter mRNA, complete cds. DEFINITION U92650 ACCESSION U92650.1 GI:2316015 VERSION

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Arabidopsis thaliana ORGANISM

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 4809) REFERENCE

Tommasini, R., Vogt, E., Schmid, J., Fromentau, M., Amrhein, N. and AUTHORS

Martinoia, E.

Differential expression of genes coding for ABC transporters after TITLE an gan haifini An gan haifini

treatment of Arabidopsis thaliana with xenobiotics

FEBS Lett. 411 (2-3), 206-210 (1997) JOURNAL

97415407 MEDLINE

(bases 1 to 4809) REFERENCE

Tommasini, R., Vogt, E., Schmid, J., Fromentau, M., Amrhein, N. and AUTHORS

Martinoia, E.

Direct Submission TITLE

Submitted (10-MAR-1997) Institut fuer Pflanzenwissenschaften, ETH JOURNAL

Zuerich, Universitaetstrasse 2, Zuerich 8092, Switzerland

Location/Qualifiers **FEATURES** 

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3 of 3